

FIGURE 1

ACTGCACCTCGTTCTATGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA
CCACCGCGTCCGGGGCGGAGCAGCACGGCCGAGGCCACTGGAGCTCCGGCTGCGTCTCCCG
CAGCGCTACCCGCCATGCGCTGCGCCGCGCCGGCGCTGGGCTCTGCCGCTTGCTG
CTGCTGCCGCCGCGCCGGAGGCCAAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACAGGGGATGGTGGACACCGCAAAAGAAGAACTTTGGCGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTAGCAGTCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCGTGGCTGCAAGCTGAAGAGCGAATCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAAGCGGAATGGCCACTGCAAGCGGAGATGGGAGCAGACA
GGGCGACGGGCTCTGCGGTGCCACATGGGTACCAAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGAAGACGTGCTCGGGCTGACCAACAGAGACTGCGGGAGTGTGAAGTGGCTGGTGC
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGGCGAGCCGCTCCCTGCAAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAGAGTGTATCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAGC
AAAACGTCTACAATACTCCAGGGAGCTACGGTGTGTGCTGCAAGGCTTCGAAGAAAGC
GAAGATGCCGTGTGCGCCGGCAGAGGCTGAAGGCCACAGAAGGAGAAAGCCGACAGCT
GCCCTCCCGAAGACCTGTAATTGTGCCGACTTACCCCTAAATTATTCAGAAGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCTGCACTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGCCCTAAACAGCTGCATTCTGGTTGTCTTA
AACAGACTTGTATTTGTATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAAGAAGC
TTGGCCGCCATGGCCCAACTGTGTTATTGCACTTAAATGGTTACAATAAGCAATAGCA
TCACAAATTCAACAAATAAGCATTTCCTACTGCACTTCTAGTTGTGGTTGTCAAACACT
ATCAATGTATCTTATCATGTCGGATCGGGAAATTAACTGGCGCAGCACCATGGCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

>**MW:** 38192, **pI:** 4.53, **NX(S/T) :** 2

MRLP RRA ALG LPL LLL PPAPEAAKPTPCHR CRGLV DKF NQGM VDTAKKN PGGG NT AWE EK TL SKY ESE IRL
L E T I E GL C E S S D F E C N Q M L E A Q E E H L E A W W L Q L K S E Y P D L F E W F C V K T L K V C C S P G T Y G P D C L A C Q G G S Q R P C S G
N G H C S G D G S R Q G D G S C R C H M G Y Q Q G L C T D C M D G Y Q G F S S L R N E T H S I C T A C D E S C K T C S G L T N R D C G E C E V G W V L D E
G A C V D V D E C A E P P P C S A A Q F C K N A N G S Y T C E E C D S C V G C T G E G P G N C K E C I S G Y A R E H G Q C A D V D E C S L A E K T
C V R K N R E C Y N T P G S Y V C V C P D G F E E T E D A C V P P A E A E T E G E S P T Q L P S R E D L

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCA ACTGCACCTCGGTTATCGATTGAATTCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCCGGAGGCCAGGCGAGCGACGCCAGCGCTAAACGGAAACA
GCCCTGCGTGGAGCTGCGAGCGCAGCAGAGTATCTGACGGCGCCAGGGTGTAGGCG
GCACGAGGAGTTTCCCGGAGGGAGGAGCTGACGCAGCAGCAGGGAGGAGCGCCCTTC
CTCGGCGCCGCGCTCTGGCTCGGAGGACATCTCTGTGCTGCTGGCACTGGGGAGG
CGGGCGCCGCGAGGAGGAGGAGCTGACCTATGGATCGTACCCAGGAAAGAGTACTCA
TAGGATTGAAGAAGATATCTGATTGTTAGGGAAAATGGCACCTTACATGAT
TCAGAAAAGCGAACAGAGAATGGCAGCTTCCATGCAATTCATTCATGAAATTTCAC
CTGGCAAGCTGCAAGGGAGGAGAATATCTATGAACTTCTGTGCTTGGCTCCCTGGATA
AAGGCATCATGGAGCATCAAAGCTCAATGTCCTCTGTGCACTGGGAACTGCGTCAAAGCA
TCAGTTGTTCAAGTTGGTTCCATGCTTGAAAACAGGATGGGTGGCAGCATTGGAAGT
GGATGTGATTGTTATGAACTGAGGACACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCACAAAGCTGAGGTGCTGATGGTTCCACGGACCTCACTGTGAGAAAGCC
TACCCCAAGCTGATGATGAGTGGAGCTTGTGACTCTGGTGTGCACTGCCCACCTG
GATTCTATGGACTGAACTGCAAAAGCAAATGCTCAACCACTGCTTAATGGAGGGACC
TGTTTCTACCCCTGAAAAAATGTTATGCCCCCAGGACTAGAGGGAGGAGCAGTGTGAAATCAG
CAAATGCCAACACCTGTCGAATGGAGGAAATGCAATTGTAAGCAGGAAATGTAAGTGT
CCAAAGGTTACAGGGAGGACCTCTGTTCAAGCCTGTCGAGGCTGTGGTGCACAT
GGAAACCTGCCATGAAACCAAAATGCCAATGCAAGGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAGGCCAGGAGGCCGGGGATCCACCTGAATCCAAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTCAACCAACTTAAGAATACCTGCTGAACTTCA
TGTTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACCTGCTGAACTTCTGTTA
TCATTATAAAATCACTGAGCTGATATTACTCTCTTAAAGTTCTGTTAAGTCTGACTCTGTAG
CATGATGTTAGATTTCTGTTCAAGTGTGCTTGGGAGCAGATTATATTATGTCATTGA
TCAGGTTAAAATTTCACTGAGCTGTTAGTTGGCAGATAATTCTCAAATACATGCAATTGTT
GCTGGGGGAGGGGAAACATCAGAAAGGTTAAATTGGGAAAAATGCTGAAGTCACAAAGAAT
TTGGATGTTGAGTTAATGTTGAAGTTACAGCATTTCAGATTGTTAGTTAGTCAGATATTAGAT
GTTGTTTACATTAAAAATTGCTTAAATTTTAAACTCTCAATACAAATATATTGACC
TTACCAATTCTCAGAGATTCACTGAGGTTAAATTGGGAAAAATTACACTGTTAGGGCTT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAAATAATGTTGAACTTTTGAT
TGGCTTGAAAGCAATAATATAATTGTAACAAACACAGCTTACCTAATAAAACATTAT
ACTGTTTGTATGTATAAAATAAGGTGCTGCTTGTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGCCCAACTTGTATTGCACTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNINHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDPGFGHGPCEKALCTRPMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTFCYPGKCI CPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCGGCGGTGCGAGAGCCAGGGAGGCCAGGGCGGAGGCCAGGCCAGGGCTGG
CCCCAGCCCACCTTCACCAAGGGCCAGGAGCCACCATGGCGCATGTCCACTGGGCCTAC
TGCTGTTGCTGCCGCTGGCCTGGCACTTGCTCTGGGCTGGGCTGGGAGCCAGGAGCTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACTGCGGGGATCCGGGACGGGAGGGCGGTACTGCCAGGA
GCCAGGACCTGTGCTGCCGCGCGTGCCTGCCAGCAGCTGTGCCCTGCCCTACCTGGGCGCCATCT
GTACTGTGACCTCTTCGCAACCGCACGGCTCCGACTGTGCTGCCCTGACTCTGGGACTTC
TGCCCTCGCGTGCACCCCTTTCCCCCATCAAGGATGTATGCATGGAGGTCGTATCTA
TCAGCTTGGAACGTACTGGGACAACGTAACTGGTCAACCTGCCAGGAGAACAGGAGT
GGCATGGTGGATCAGACATCAAAGGCCATCAACCGGGCAACTATGGCTGGCAGGGTGG
GAACACAGCGCCTCTGGGCATGACCTGGTGAGGGATTGCTACCGCCCTGGGACCA
TCGGCCCATCTCTCGGTATGACATGATGAAATTATAACAGTGGCTGAACCCAGGGAG
GTGCTTCCCACAGCCCTCGAGGCCCTGTAGAAAGTGGCCAACCTGATTCTATGAGCCTCTGA
CCAAGGAACTGTGCGAGGCTCTGGGCCCTCCACAGCAGCTGTGGCATCGATGTGCT
CAATCCATTCTGGGACACATGACGCCCTCTGTGCCCCAGAACCTGCTGTCTTGTC
ACCCACAGCGGGCTGCCGCGTCTCGATGGTGCACCTGGTGGTCTCTGGCTCG
CGGAGGGCTGGTGTGACCTGCTACCCCCCTCTCGGGCGTGAACGAGACGAGGCTGGC
CTGGCCCTCTGTATGATGACAGCGAGGCCATGGGCGGGCAAGGCCAGGCCACTGCC
CACTGGCCCAACAGCTATGTTAAATAACATGACATCTACCAAGGTCATCTCTGTCTACCGCC
CGGCTTCAACGAGGAGATCATGAAGGAGCTGATGGAAATGGCCCTGTCCAAGGCCCTA
TGGAGGTGATGAGGACTCTTCTTACAAGGGAGGCATCTACAGGCCACAGGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACCCCGGCTGGGACCCACTCAGTAAGATCAAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCCACTGGGACTCTGGGCCAACTCTGGGG
CAGGCTGGGGCGAGAGGGCCACTTCCGATCTGGCGGGCTGAAGGAGCATGGGTCATCACTGAGGCTG
AGCTTCTGTGCTGGCGTCTGGGCCGCGTGGGATGGAGGACATGGGTCATCACTGAGGCTG
CGGGCCACAGCGGGGCTCCGGCTGGGATCAGGCTAAGGGCGGGGAAGAGGCCCCAATG
GGGCGGTGACCCCCAGCTCGGGCACAGAGCCGGGGGCCAGGGCGGCCAGGGCGTCAAT
CCCGGCCGGGTTCCGCTGACGCAAGCGGCCGCTGGGAGGCCGGGAGACTGGC
GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCCTGGGCTGGGAAGAGCACAGCTGCAG
ATCCCGGGCCTCTGGCGCCCCACTCAAGACTACCAAGGACACTCAAGTCTCCAGC
CCCAATCCCCACCCCAATCCGTTTCTTTTTTTTTAGACAGGGCTTGTCTCC
TTGCCAGGTGGAGTCAGTGGCCATCAGGCTACTGTAACCTCCACTCTGGGTTCA
AGTGACCCCTCCACCTCAGGCTCTCAAGTAGCTGGGACTACAGGTGACCCACACACTGGC
TAATTTTTGTTATTTTTGTTAAAGAGGGGGGCTCACTGTGTTGCCAGGGCTGGTTCAACT
CTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGGATTGCAAGGATGAGCC
ACTGCAACCCAGGCCCTGTTATTTTATTCTCAGATTTTTCTTCACTGTTAAAA
TAAAACAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTCTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCCAGAACCTGCTGTCTTGTAACCCAC
CAGCAGCAGGGCTGCCCGCGNTGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCCTGCTACCCCTTCTCGGGCGTGAACGAGACGAGGCTGCCCTGGC
CCCCCTGTATGATGACAGCCGACATGGTCGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTGGCTC
CAAAGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGGCCAGGCAGTCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGG
GAGCAGTGCCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTGAACCTCGTGG**ATG**ACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCAGCTGTGCAACGCCAGCGGGGCCATGCCTGCAGCCGGCTGCCGCATCCTT
GCCGCTGCTCCCTGCACTCGGCTGCTGCTCTGGGACCCGGCAGCTATAGGCTCTGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTG GCCACTCCTCACAGACCTG
GCCAGTGGGAGCCTGTCCTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGCCCCACCTGACCCCTCCATGGCCTCTCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCTGTGCTCAGGCACCTCTCCCCAGGAAGCCTT
CCCTGCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCACT**TAA**AGGCTGAGATGAAGTGGACTGAGTAGAACCTGGA
GGACAAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

□ □ □ □ □ □ □ □ □ □

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCFHGPATLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRCQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGCAGATCCGCGAGTACCAACTCTACAGCAGGACAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGGCCAGGGACGGCAACAAGTTGCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGGAAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGCCCTTCAGAACGCCCGGACGAGG
GCTGGTTCATGGCCTCACGGCGAGGGGGGCCCGCCAGGCTTCCCAGCCGCCAGAAC
CAGCGCGAGGCCACTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGCAGCTCGAGTTGTGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGGGCCCCCAGCCCCCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCCTCCC
CCCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCAAGCATTGAGCCCCCTCCGGACGGGTGGCAGGCCCTGGAGAGGA
CCCCAGGGCGCTGGCACAGTGGCCCTCCAGCTGGGAGGGCTCTGAAGCC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCCTGAGACAACCGCTGGAGGGCTGTGCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCAACTCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGAAAAAGAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

 **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGACATGGAG
GACAGCAGAAAGGGCAACACAGGCTGATAAGACCAGAGCAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTCCTCTAGCTGGAGTCTGGACTTCACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCTTTCCCACCCATTGATTTTAT
TTCGGTACTTCAGAAATGGCCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTTCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTACTCAGGTGTCACAGGCTCAA
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTTGACCTCAGT
CCTCTGGGATCCCGGAGGGCTAACCTCTACCTCCACAAACAACCAATTAAATAATGC
TGAGATTCTCGAGAACTCACAATGTAAGCTCGGTGACACCGTCTACCTGATGGCAAC
AACTGGACGAATCCCCATGAACCTTCCAAGAAATGTCAGAGTCTCATTGAGAAAAC
AATATTCAAGACCATTTACGGGCTGCTTGCCCACTCTTGAAAGCTGAGAGCTGACAC
GGATGACAACCTCATCCAGTGGGGGGTGAAGACGGGGCTCCGGGAGGCTATTAGCC
TCAAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCGACATGCCCTTCAGAA
TCTCTGGAGCTGGAGCTTATTGTCAGGAGGAAACCTCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCATCTACCAAGCTCAAGGAAATTCTCAATTGTAACGTAATTCTGCTC
CACCCCTCTCCGATCTCCAGGTACGCATCTGATCAGGCTTATTCGAGGACAACAGAT
AAACACATTCTTGACAGCCTCTCAAAAGTCTCGTAAGCTGGAGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGGTTTTGATAATCTCTCAACCTGAAAGCAGCTC
ACTGCTGGAATAACCCCTTGACTGAGCTATTAAATGGGTCAAGAATGGCTCAA
ATATATCCCTCATCTCAAGTGCGGGGTTCATGTCAGGCTTGAAACAAGTCCGG
GGATGGCGTCAAGGAATTAAATGTAATTGTCCTGCTGTTGGGCTTGAAAGCTGG
CCTCTCTCACCCAGCCCAAGTACAGCTCTCCGACCATCAGCCTCCACCCCTCTCAT
TCAAAACCTAGCAGAAGCTACACGCTCCAACTCCTACACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGGTGACGGGACCCATTTCTGAAACGGATCCAGCTCTCATC
CATTTGTAATGATACTTCAGTCAAGTCACTGGCTCTCTCTCACCGTATGGCATA
CAAACCTACATGGTGAAATGGCCAAGGTTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACTGAGGCTGTTAACCTTAGAGGCCGATCCACCTATCGGATT
TGTGTTAGTGCACACTGGATGCTTTAACCTACGGCGCGGTAGAAGACACCATTTGTTGAGGG
CACCAACCCATGGCCTCTATCTGAAACAACCGCAGCAACACGGCTCAGGCTATGAGCAGCG
CGTCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTGATGGGGCGCGTGTATATT
GTGCTGGTGGCTTGCTCAGGCTCTTGTGGCATATGCAACAAAAGGGGGCTACACCTC
CCAGAAGTGGAAATAACACGGGGCCGGGGAAAGATGATTATTGGAGGGCAGGCACAAAGA
AGGACAACCTCATCTGGAGATGACAGAAACCACTGTTCAAGATCGCTCTTAAATAACGAT
CAACTCTTAAAGGAGATTCAAGACTGCAACGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCACAGCTGGAGC
ACTGCCATAGTGAAGCCAGAGGCCAGCGTTACAGGGGGCAATTAGACTCTTGAGAA
CACACTGTTGTGTCACATAAGACACCGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGATTTGAATACTCTGTAATTATACGGGTGACTATATAATGGGATTAAAAAAAGTG
CTATTTCTATTCAAGTTAACACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVS KLLACPSVRCDRNFVYC NERSLTSVPLGIP
EGVTVLYLHNNQINNAGFP AELHNVQSVHTVYLYGNQLDEFPMNL PKNVRVLHLQENN IQT
SRAALAQLLKLEELHLD DNSI STVGVEDGAF REAISLKLFLSKNHLSSVPVGLPVDLQELR
VDENRRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRN SLSHPPD
LPGTHLIRLYLQDNQINHPI TAFSNLRKLERLDISNNQRLM LTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYI PSSLNVRGFMCGPEQVRGM AVERLN MNLLSCP TTGPLPLFTP
APSTASPTTQPPTLSIPN PNSRSYTPPTPTSKLPTI PDW DGRERVTPP ISERIQLS IHFVN
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICL VPL
DAFN YRAVEDTICSEATTHASYLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFV LVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGT KKDMSILEMTSFQIVSLNNNDQLLKG
DFRLQPIYTPN GGINY TDCHIPNNMRYCNS SVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTQTALESSCENKRADLVII
DSSRSVNTHDYAKVEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPVRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGVGQVDFNTLKSIGSEPHEDHVFVLVANFSQIETLTSVFKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYLILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCRKAVIDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNKGTCRVHDCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCPEGYIILEDGKTCRRKDVCQAIDHGCEHIJVNSDDSYTCECLEGFRILA
EDGKRCRKAVIDYCASENHGCEHECVNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRFNFSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAIAEDFSTMDEISEKLKKGICEALEDSDRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEDDNLLRSTQKLSHSTKPGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCCTCGGCCAGGGAGGGC
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCCTGGACTCCGTCAGGGCCAGGGAGGGC
CATGATT TCCCGGGCCCTGGTACCAACTTGCTCGGGTTTGTTCCTGGGCTGA
GTGCCCTCGGCCCTCGGGGCCAGCTGCACTGCACTTGCCGCCAACGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTTGCACTGGGAGGGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAAGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAGCAAATCTAGGGGCCACAGCATCAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCTCCATCTGGCTCTCAGGGTGTCCCCAT
GTGGGGCAACCGTACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCAAATACCA
GTGGGATCGGCAGCTCCATCTTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAAGCCTCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCAGGCCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTTGTGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACGCCGGGCAAGGCCCTGGAGGAGGCCAGCAAATGATACTCAAGGAGGATGCC
ATTGCTCCCGGACCCCTGCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCC
TTCTCTGTACCTCCGCAGAGCCCTGGGCCACCCCATGGCCCTCCAGGGCTGGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCCAACCAATATCCCCATCCCTGGTGGGTTCTTCTCTGGCTGAGCG
CATGGGTGCTGCTGTGATGGTGCCTGCCAGACTCAAGCTGGCTCTGGTAT**TGATGAC**
CCCACCACTATTGCTAAAGGATTGGGTCTCTCTTCTATAAGGGTACACCTCTAGCAC
AGAGGCCAGTCATGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCACTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGATTGGAGGAGCCCTACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTCAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGGATCTC
TTATTAAAACATAACATGAAATATGTGTTGTTCTATTGCAAAATTAAATAAGATACTAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSR
MGAAPVPMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCA~~ATGAA~~ACGCCTCCGCTCCTAGTGGTTTTCCACTTTG
TTGAATTGTCCTAATCTAAATTGCAACAGACACCTGTCTCCAAATGCAAATGTAA
AATACGCAATGGAATTGAAAGCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCACTCCTGTGCGAAAATGCTAATTG
ACTAACACAGAAGGAAAGTTATTGTGATGTGACCTGGCTTCAAGATCCAGCAGTAACCA
AGACAGGTTTACTAAATGATGGAACCGTGTGATAGAAAATGTGAATGCAAACGTCATT
TAGATAATGTCGTATAGTCGAAATATTAAATAAAACTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTCAAGAAGCTATAAGAAAATCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATATTAGCTGAATCATCTCATTACTAGTTACAAGAACACA
CTATCTCAGCAACGGACACCCCTCACTAACTTCAACTGAAATTGTAACCGTGAAT
AATTGGTCAAGGGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTCAGGAAACTCATGCAACTGTGACAAGCTTTAAAGGATATCCCAGAGCTTC
AAAAGACCCAGACAGTTGTACAAATTCAACGGGATATGCTCTAAAGTTCTTTGTAT
TCATATAACATGAAACATATTCTCATATGAATATGGAGACTACATAAAATATT
TCACAAAGAGAAAAGCTGATGATTCAATGCAATGAGCACCTCATGCCGTGATACCT
AGAGTATTGGCTTTGCTTCTCATCTGACAACCTTCTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGACTCATATCTTCAGTAATTCTCAGTCATGAGCTAAACCC
ACCCACATTATGAACTTGAAGGAAACATTACATTAACTAGTCATGAAAGGTACAGATA
GGTATAGGACTTATGTGATTGGAATTACTCACCTGTACATGGGATATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAATGAGCACCCACACCTCATGCCGTGATACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTAACTGAAATTAAATTCTACTGATTGTCATGCTTGGCATTGCAATT
ACCTCTGGTTCTCGTGAATTCAAGCACCAGGACAAACATTCAACAAATCTTGTCTG
TAGGCTATTCTCTGCTGAATTGTTCTTCTGTGGGATCAATAACAAATACTAATAAGCTCT
TCGTGTTCAATCAATTGCGGAGCTGCTACACTACTCTTCTTGTGCTGATTGCAATTG
ATTGAAGGCATACATCTCATCTCATGTTGTTGTTGTCATCTACAAACAAAGGATTGG
CAAGAATTATTATATTCTGGTATCTGGCATTCAGGCGCCTGGTAGTTGGATTTCGG
TAGGATACAGATATTATGGCAACACAAAGTATGTTGGCTAGCACCAGAAACACTTATT
TGGAGTTTATAGGACAGCAGTCATGCTTAATTCTTGTGTTAATCTCTTGGCTTGGAGTCAT
CATATAACAAAGTTTCTGTCACACTGCAAGGGGTTGAAACCAAGGTTAGTTGCTTGG
TAAGGTCTTGCAAGAGGGAGCCCTCGCTCTGTTCTCTCGGCACACCTGGATCTT
GGGGTCTCCATGTTGCAAGCAGTCATGTTGTTGCTACAGTCTTCAAGTCAGCAATGC
TTTCCAGGGGATGTTGCTATTCTTATTCTCTGTTTATCTAGAAAGATTCAAGAAAGAT
ATTACAGATTGTCATTAAATGTCCTGTTGTTGGATTTAAGGTAACATAGAGAATG
GTGGATAATTACAACACTGCACAAAATAAAATCCAACTGTGGATGACCAATGTAAAAAA
TGACTCATCAAATTATCCTAAATTAACTACTAGACAAAAGTATTAAATCAGTTCT
GTTTATGCTATAGGAATTGATGAAATTAAAGGTTAAATTATGATCATATAGATAACTATGT
TTTCTATGTAAGGAAATTGTCGAAATTAGTATGCACTGAGATATTGGAAAGTATTGGTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTCTAACACGGAGAATGTATGAA
TGTCTGAAAGGAAACACTGCGCTGATATTCTGTGACTCGTGTGCTTGGAAACTAGTCC
CCTACACCTCGGTAATGAGCTCATTACAGAAAGTGGACATAAGAGAATGAGGGCAGA
ATATCAAACAGTGAAGGGAAATGATAAGATGTTGAAATTGAACTGTTCTGTTGAA
TAGCTGAGAAAATTGTCGACATAAAATGAAATTGAAAGAACACATTACCTTACCAATT
TTGTTCTGAACTTAAATGTCACAAAAACATTAGACTCTGTTGCTAAATCTGTTCT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTCEDDNEC
GNLTOSCGENANCNTTEGSYCMCVPGRSSSNQDRFITNDGTCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSLTLEFVKTVNNFVQRDTVVWDKLSVNRRTHLTKLMHTVEQATLRIQSOFQKTTEDT
NSTDIALKVFFFDSDYNMKGHIHFMNMMDGYINIFPKRKAAVDNSGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEERVISSVISVMSMNPPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFFWWFFSEIQRSTTITHKNLCCSLFLAELEVFLVGINTNTNKLFCSTIAGL
LHYFFLAFAFWMCIEGIHLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLAFGVIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTTWIFGVLVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCAGTCAGTCAGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAGATTATAATTTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTTACCTTC
TGGTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCG
CTAAGCAGGCCCTCTCCCTCCCGCAGATCCGAAACGGCTGGCGGGGTCACCCCGCTGGGA
CAAGAACGCCGCCTGCCTGCCCTGGGGCCGGGGAGGGGCTGGGGCTGGGGCTGGGGAGGGCG
GGTGTGAGTGGGTGTGCGGGGGGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGCACCTACCCGTGGGGCCCTAAGGCCACTATATAAGGCTGCCGGCCGGAG
CGCCGCGCCCGTAGAGCAGGAGCGCTGCCAGGATCTAGGGCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCCGCCAGCCTCCGCACCCCATGCCGG
AGCTGCGCCGAGGGCCAGGGAGGTGCG**AATGCGGAGCGGGTGTGGTGGTCCACGTATGG**
ATCCTGGCGGGCTCTGGCTGGCGGCCCTCGCCTCTCGGACGCGGGCC
CCACGTGCACTACGGCTGGGGCACCCATCCGCCCTGCCGACCTGTACACCTCGGGCCCC
ACGGGCTCTCAGCTGCTTCTGCCATCGTCCGACGGCGTGTGACTGCCGCCGGGC
CAGAGCGCGCACAGTGTGGAGGATCAAGGCACTCGCTCTGCCGACCCGTGGCATCAAGGG
CGTGCACAGCGTGGCTACCTCTGCATGGGCCAGCGCAAGATGCGGGCTGCTTCACT
ACTCGGAGGAAGACTGTGTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGACCGA
TCCGAGAACGCTCCGGTCTCCGTGACGTCGACGGGAGCTGTAACAGAA
CAGAGGTTCTTCACTCTCATTTCTGCCATGCTGCCCATGTTCCCAGGGAGCTG
AGGACCTCAGGGGCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTGTCAACCGACTGGAGGGCGTGAGGAGTCCCACTTGAGAAGTA~~ACT~~
GAGACCATGCCGGGCTCTTCACTGTGCTGCCAGGGGCTGTTGACCTGAGCGTGGGGAGC
TGCTTCTACAAGAACAGTCTGAGTCCACCTCTGTTAGCTTAAAGAAAATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT
CATAAACATTGTAAGCTGTAGCTTGGCCAGCTGCTGCCCTGGGGCCCCATTCTGCTCCCTCGA
GGTGTGGACAAAGCTGTGCACTGTCTCAGTTCTGCTTGAATACCTCATCGATGGGGAC
TCACCTCTTGGAAAAAAATTCTTATGTCAGCTGAACTGAAATTCTCTAATTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCACTGAGTTTAATTTCAGGAACAGGTGATCCACTCTGTA
AAACATGGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTACTTCAGGG
ACCATTGGCCCTTCCCAAATCCCTCCAGGGCAGAACACTGACTGGAGCAGGATGCCAACAG
GCTTCAGGAGTAGGGGAAGGCCGCTGGAGGCCCACTCCAGCCCTGGGACAACCTTGAGAATCCCC
CTGAGGGCCAGTTCTGTCATGGATGCTGTCTGGAGAATAACTTGCTGTCCCGGGTGTCACTG
TCCCATCTCCGCCACGCCCTCTGCCACCTCACTGCCCTCCCATGGATTGGGGCT
CCCAGGGCCCCCACCTTATGTCACCTGCACTTCTGTCAGGAAATTGAGTAAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCTAAATTATATTATGTCAGTGTAACTGAGGTTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCCAGAAGTTCAAGGGCCCCCGGCCTCTGCGCTCCGGGACCCCTGACCTCTCA
GAGCAGCGGCTGCCGCCCCGGAAAGATCGCGAGGAGGAGCCGCCACCGCCTCCTCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGTATCATAAGGCATGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAACTGGTCGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGGAAATATCGTTGTAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGACCAACAGCTCATCACAAATGAATAACAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGGTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGCTAGTAGTTGTGGCCTTAGTGATTCGGCTTGTTGTGGCTATGCTAT
GCTCAGAGGAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAACTCCAGCACTTGGAGG
CCGGCGGGCGGATCACGAGGTAGGAGTCTTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATAGCTGGCATGGTGGCATGTGCCTGCAGTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA
ATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRLYLVVALGYHKAYGFSAPKDKQQVVTAVEYQEAIACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPRLGSQST
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVIISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAAATCCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAGAAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACGCCGGACCTGGCAT
CATGCTGTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTCTAAATAA
ATGAATTAATCTCTATGACCATCTATACATACTCACCCTCAAAAAGTACATCAATA
TTATATCTTAAGGAAATAGTAACCTTCTCTCTCAAATATGCATGACATTGGACAATG
CAATTGTGCACTGGCACTTATTCTCAGTGAAAGAAAATCTTGTGGTCTATGGCATTCA
TTTGACAAATGCAAGCATCTCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG
TGGAAATCTTAAGGGGCCATTACATTCTGAGGAAGAAGCTAAAGATGAAGGCACATGCCACT
CGAACATTGCTACTGGCTTAGCTACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCACGGTTATGACCTGTGAAATCAGGCCCTGGTTACACCCAGATCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTTCCAGCCAGATTGCC
AGCTAACACAGATCTCTCTCACAGACTAACATAATGCAAAAATATTGAAATCTCACAG
ACTTCCAGTAACCTTACTGGCTGTGATTATCTCAAAACATAATTCTCAGTCACCAAT
ATTAATGTAAAAAGATGCCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCATGAAACATGCTGTCGCAACTGACGAAACTTACAGAAACTCTATATTAACTACA
ACTGCTTCTACATACTCAGCTGACCTTATTGCGCTACATAATCTCTCGACTTCATCTC
AATTCAAAATAGATTGCAAGATGCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCGTGATGATTGGGAAATCAATTATCAGAAATCAAAAGACATGAACTTTAAGCCTTATCA
ATCTTCGAGCTGGTTATAGCTGGTATAACCTCAGAAAATACCGATAACGCCCTGGTT
GGACTGGAAAATCTAGAAAGCATCTCTTTTACAGAACAGCTTAAAGTACCCCAGT
TGCTCTCAAAAGTGTAAATCTAAATTGGATCTAAATAAAATCTTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCC
GAGCTGATTCTCATCGATAGTCTTGCTGTGATAACCTGCCAGAATTAAAGAAAATAGAAGC
TACTAACACCTCTAGATTGCTTACATTCAACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AACTCACTCATGCTGAAAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGATCTCTG
CCAAACCTCAAGGAATCAGCATAACAGTAACCCCCATCAGGCTGTACTGTCTCCTGG
GATGACATGAAACAAAACCAATTGCGATTCTGAGGCCAGATTCACTGTTTCCGGGACC
CACCTGAATTCAAGGTCAAGATGTCGGCAAGTGCAATTTCAGGGACATGATGAAAATTGT
CTCCCTTATAGCTCTGGAGGAGCTTCTCTAACTTAAATGCTAGTAAAGCTGGGAGCTATGT
TCTCTTCACTGTTAGGACTCTAGCAGAACCCAGCCTGAAGATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCTCTGACAGACAAGTTCTATGTCATTCTGAGGAAACACTA
GATATAATGGCGTAACCTCCAAAAGAAGGGGTTTATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAAATG
GCTCTTTGAATATTAAAATAGAGATATTCAAGGCCATTCTAGTTTGTGCTGCAAGCA
AGTTCTAAATCTCAAATCTAGTGTAAATGCAAGCCTTGTCAAGACTGAAAATCTCA
TGCTGCGCAAAGTGTGCTGAATACCATCTGATGTCAAGGTATAATCTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTTATGATATTCCACCATCTATCAGAAAACAGAAAAAA
TGTGTAAATGTCAACACCAAAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGATAATAC
CACAAACACTTATGGCTGTCTGGAGGCCCTCTGGGGATTATTGGGTGATATGCTTATCA
GCTGCCCTCTCCAGAAAATGAAACTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCTCTCTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGCTCT
AAAAACACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSNLQELYINHNLLSTISPGAFIGHHNLLRLHLNSNRQLQMINSKWFDA
LPNLEIILMIGENPIIRIKDMNFPLINLRSVLVIAGINLTEIPDNALVGLENLESISFYDRL
IKVPHVALQKVVNLIKFLDLNKNPNIIRRQDFSNMLHLKELGINNNPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGGSYVFPHCRATAEPOPEIWITPSGQKLLPNTLTDKFYVHSGETLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSVKWTAFV
KTENSHAAQSARIPS DVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQE
YEKNNTTTLMACLGLLGIIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCCTTGTAAACACGCCAAGAAGGAATCAATAGTGTGACAGGGCTGAACTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGTCGACATTCCAGCATGAATCT
GGTAGACCTGTGTTAACCGCTTCCCCTCATGTGTCCTCTACAAGTTGTTCTTA
TGATACTGTGCTTCATTGCCAGTATGTCCTAACAGGCTGTTGTTCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAATACCTAGAGATCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTCTCAACCTGCTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCCTCAAAGGAGTAGCTGAAACCTTGCAAGACTCTGGACTTGTCGACATGGATTCAAAG
TGTGCACAAAAATGCCCTCAAAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCCACTGTACTCTACAGCAAGTTCTGAGGACATGGCTCCAATCATGAGACAGCCAC
AACGTGATCTGAAACCTGCTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTGTATCTCATATGTTGATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGAACCTCGAAACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGTTATGTGCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAACATTGAA
ACTTTGTATTTCACTTTTGAAATTATGCCACTGCTGAACTTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFLMILCFHSASMCPKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHEAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGAGATGCAAGGTGAGCAAGAGGAATGCTGGCGGGGG
GGCTGAGGAGCATGCCAACCCCCCTCTGGCTCTGGCAGCCCACATCCTCTGTGTTGCT
GGGCTCAGTGTCTGTCAGGCTCGGCCAACGGCTGGCCCGGGCTGCGAGTGCTCCGGCCAGG
ACCGCGCTGTGCTGTCCACCCGAACTGTTGTGGCAGTCCCCGAGGACATCCCCACCGAG
ACCGCGCTGTGGACTAGGAAGAACCGCATCAAACGCTAACCCAGGAGCAGATTGGCAG
CTTCCCCACCTGGAGGAGCTGGAGCTAACGAGAACATCTGAGGCCCTGGAGGGCCGGC
CCTTCACACCTCTCACCTCCGGACGCTGGCTCTCGCAGAACCCGCTGAAGGCTCATC
CGCTGAGGCTCTCACTGGCTTCAGAACCTGACCAAGGAGACATCAGCAGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGC
ACAATGACCTCTGTCATACATCTCACCGCCCTTCAGCGGCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAACATGCAACTGCTTCCATCCCCACCGAGGCGCTGCTTCCACCTGCAACGGCT
CATCGTCTGAGGCTCGGCACCTCAACATCAATGCCATCGGGACTACTCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCCACTGGCCCTACTTGACACCTGACACCCAA
TGCCTCTAGGCCCTCAACCTGAGCTCCCTGTGACATCACACATGCAATCTGACCCTGTG
CTACCTGGCCCTCCGCCACACTGCTATCTGGCTTCCATCAACCTCTCCTACACCCATCA
GCACCAATTGAGGGTCCATGTTGATGAGCTGCTCGGCTGCAAGGAGATCCAGCTGGTGGG
GGGCAGCTGGCCCTGGTGGAGGCCATCTGGCTTCCGGCCCTAACTACCTCCGGCTGCTCAA
TGTCTCTGGCAACCGACTGACCAACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTTCAACCCGCTGGCTCTGGCAGACTGTCGGCTCTGTGGTGTCTGG
CGCCGCTGGGGCTCAACTCAACCCGAGCAGGCCACGGTGGCCACGCCAGGTTTGTCCA
GGGCAAGGGTCAAGGACTTCCCTGTGACTCTGGCCAACTACTTCACTCTGGCCGGCG
CCCGCATCGGGGACCCCAAGGGCCAGCAGGGTGTGACCTGGAGGCCAACCGTGGAGT
GTGTGCCGGCCGATGGCAGCCGCCGCCCCCATCTCTGGCTCTACCCCGAAAGCACCT
GGTCTCAGGCAAGGCAATGGGGCTCACAGTCTTCTCTGTGATGCCAGCTGGAGGTGGC
ACGGCCAGGATCACGGACAAAGCCACGTACTGTGCACTGCCAGCAACGCCGGCGAACAGAC
TCTCATGGCCGCCACTCTGCACTGTGCGCAGACTCTGCCAGCTGGCCCATCAGCCCAA
GACCTTCGCTTCTACATCCAACAGGGGGAGGGAGAGGCAACAGCACCGCGCCACTG
TGCCTTTCCCCCTGACATCAAGACCCATCATGCCACCCACATGGGCTCATCTTCTTC
CTGGGGCTGTGCTCTCTCTGGCTCTGGCTGTTCTCTGGAGGGGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGATCGAGTATGTGCCCGAAAGCTGGAGCAGGACATCAGCTCCGG
ACGGCGCCCGCAAGTTCAACATGAAGAGATGATATGAGGGCGGGGGGGGGAGGGACCCCG
GGGGCCGGGGAGGG
CTCTCCACCCCTCAACACAGTCTCTTCTCTCCCTCCCTGGCTCTACCTCTCAGTCTGGCTTCC
CCAGGCCCTACCCACCTGCCCTCTTCTACAGGACCTCTAGAAGGCCAGACCTGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGAGCAACCCGGCAGAGTC
ATAATTCAATAAAAAGTACGAACATTCTCTGTAACTGGGTTCAATAATTATGGATT
TATGAAAACCTGAAATAAAAAAGAGAAAAAAACTAAAAAAACAAAAAAACAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPETTRLLDLGKNRIKTLNQDEFASFPHLEELMENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHINAINARDYSFKRLYRKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVPEPYAFRGLNYLRLVNVSGNQLTLEESVFHSVGNELETLLDSNPLA
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGEFKDFPDVLLPNEYTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAIWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFFPDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIIEIYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGACCTGGCCCCGGCTCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGGCCAGCC
AGGGAGCGGGCCGGGAAGCGCGATGGGGGGCCCAGCCGCCTCGCTCCTGCTCCTGC
TGTCGCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCTGG
ACATCTGTAAACAGTGGTGGCTGGCACCGTGGTCAAGTCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCTACGCCACAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGCAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAAGTCCAAGTCCTCGTCACTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAATCTTCAATTACGGAAAAAGACACGCCACCTAAACTGTCACTTCTGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCAAGAACACCAGC
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCACTGGTACATTCCAGGTTACCC
GGGAGGATGATGGGGGAGCATTGTGCTCTGTGAACCATGAATCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTGCTACACTGTGAGGGTCCGGCAATCCAGTCC
CCCAGCAGTACCTATGGAGAAGGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCTCAACAAGAGTGAAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGAGCTACAAGGCCACTACACCCCTCAATGTTAATGACCCAGTCCGGTCCCT
CCTCCTCCAGCACCTACCAGCCATCATGGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGCAGCGGACACGGCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGAGCACAAGAAGGAATATTCATCTAGGGCGCTGCCACTTCTGC
GCCCCCCAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCGCCCTCCGCTTCTCCAGCCACCCACCCCGTACAGAATGCTGC
TTGGGTGCGTTTGTACTCGGTTGGATGGGAGGGAGGGAGGGGGGGAGGGAGGG
TTGCCCTAGCCCTTCCGTTCTGCTGATTTGGTTATTATTATTTGTAAACATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAA\$LLLLL\$FACCWAPGGANLSQDDSQWPWSDETVVAGGTVV\$LCQVKDHE\$SLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSISISNV\$ALADEGEYTC\$IFTMPV\$RTAK\$LV
TVLGIPQKPIITGYKSSLREKD\$ATLNCQSSGSKPAARLTWRKGDQELH\$EPTRIQEDPNGK
TFTVSSS\$TFQVTREDDGASIVCSVNHE\$LK\$ADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWE\$EGSV\$PPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSS\$TYHAIIGGIVAFIVFLLLIMLI\$FLGHY\$LRHKGTYLTHEAKGSDD
APDADTAIINAEGGQ\$GGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGTTAGGGAGGAATCCACCCCCCACCCCCCCTTCTCTCTTCTGG
CTCGGACATTGGACTAAATGAACCTGAAATTGTGTCGAGGATGGTCCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTG
GCTGGAGACGCTCTTTGTCGCTGAAACGTTACAGGGACGTTGCAAAGAGA
TCCTGTTCTGCAATGAGATAGAAGGGGACCTACAGCTGAGAATGGCTTCACA
AGTCAGCGCTTCACTGCCGCAGTTCAGTTACATTTATCTGATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTCGTAACCTTTATAATGCGTTAGTTG
CAAAGAGAAGGGCTTCAGTAACTGTTCCGGGGCTTTCTGGGCTGCA
AAACAAATGGCTTCACTGAAACGTTGAGCTGGGAGCTGGGCTGAAAGG
CTGACATCAACAAACAAGATCAAGTCTTCAGAAGCAGACTTTCTGGGCTG
CTGAAATATCTCAGGCTGATTAAATTATTACAGAGATATAGACCCGGGCTT
CTCAGGACTTAAATGACAACTCTCATCAGCACCCCTACCTGCAAC
GTGTTCCAGTATGCTCCCATCACCCACCTGCACCTCCGGGTAACAGGG
CTATGAGGAGGCTTGGAGCAATCCCTGGTATTGCGAGGATCCTG
GGGACTGCACTGTGATCTGCTCTCCCTGAAAAGAATGGCTG
AAACATCCCAAGAATGCC
CTGATCGCCGAGTTGCTGCAAGGACCCACAGCTGCAGGGTAAAGACCT
CACCGGAACAGGACTTGTCTTGGAGAAGGGCTTCAAGTCTCCGGCG
CCCAAGAAGAGAACCTTGTCTTGGACCCCTGCAACTCTTCA
GATCAGGCCACACCAGGGCTGCTCCAAACCGAGGTAACAGATCCCAG
AAACATCAGAGGACAGCAGGATAGCAGGGTAGCTGCAGGA
AAACATCCCAAGGTTAAAGATGAC
TCAACACAGGAACAGTGAGCAGCTGGCTGATTGAGGCCAAGCT
GCTTCTTCACTGAGATAACAGATCCACAGCATCCGAAATC
ACCTCATTCTGGGATCTGGCAACATAATCCTGACTGT
AACCTTTGGACACTCAGGTGGCTATACATGGATAGCA
AACTGGACAGCCTGCTGCAAACCTAGAGTACCTG
GAAATTCCGGGGCTGCAAACCTAGAGTACCTG
GAGCTGGAGTAAACGCTATCCAGCTCA
TCCTCCGGGACTTCACTGCACTGGCA
CTGAGGTCCCTGCTGAGCTGGACCTGCTGGGGTCTCG
CAATTACTTCACTGACCTCCGGTGGCAGGGTGT
TAGACCTCCAGGAAACCCCTGGAGTGTCTC
GAAGCCTTCAAGCTGAGGGAGCTCAAGTGT
GAAGCAGCCGGTGAACCTT
GAACGCTGGGGTCCGAAGTGTGATGAGGCCA
TAGAAGGATTCTAGCTCTCTCCAATGAGAGACTGCC
CGCCCACTTAACCTGGCAGTAAACAGCAG
AACTCTACCTAGACACAGCAGGGTGT
GTTGTCACTCCGGCTTCACTGGGGTGGCAT
GGTCAAGAGACGAGATGCCA
GACTCTCTCACTGGCTCTCAGACTAA
GACTGGCTTCAACAGCAGATGGGGCC
TGGCTCTCACTGCTCTCAGACTAA
ATACATCTTCCCCACCGCAGG
CCATCAGCTGGATGGCATAAGT
GACCCCTTACTTAGCTCCCTCC
GACCCCTTACTTAGCTCCCTCC
GACAGCTGGCTTCACTGGGGTGG
AACTGACAGTGCCTCGCCCTCG
ATATATACATATACACATCT
CCCCGTGATGGCTCCCTG
TGTAAATAAGTAACCTGACTCTGAC

FIGURE 34

MLLWILLTSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLLHMENNGLHEIVPGAFQLVVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPAGFQDNLNKLEVILLNDNLISTLPANVFQYVPITHLDLRG
NRLKTLFYEVEVLEQIPIGIAEILLEDPWDCTCDLSSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDNLNETTEQDLCPKRNVRDSSLAPPQAQETFAPGPLPTPFKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAITGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLK
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFLAGLNQLEYLNVEYNAIQLILPEGTTFNAMPKLRLILLNNNNLRLRSLPFDVFA
SKLSLHNHYFMYLVEAGVLQDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPLTSHSKNSTGLAETGTHNSYLDTSRVSISV
VPGLLLVPVTSAAFTVVGMLVIFLRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLS

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTGACCCGGCGCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC
TGCAACGGGGCTGGCAGCGCTCGCACACATTCTGTGCGGCCCTAAGGGAAACTGTGGC
CGCTGGGCCCGGGGGGATTCTGGCAGTGGGGGTCGTCGGGAGCGAGGGCGGAGGG
AAGGGAGGGGGAACCGGG
AGCTCTGGCTCTCGAGCGGCACAGATCCAAGGTGGGAGCAGCTCTGCGTGCAGGGGG
AGAATGAGGCCGGCTTCCGCCCCCTGTGCTCTCTGCGCAGGGCTCTGGGCCGGGG
CGCGAACACCCACTGCGCACCGTGTGGCTGCTCGCCTCGGGGCTGCTACAGCTGC
ACACGGCTACCATGAAGCGCAGGCCAGGGCCAGGCTGACCTCTGCGAGGGGGGG
AGCAGCGTGCCTGGGCCCGAGCTCGCGCTGTGCTCGCCTCTGCCGGCAGGCCAGG
GCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCCACT
GCACCCCTGGAGAACGAGCCTTGGGGGTTCTGGCTGCTCCGACCCCGGGGCTC
GAAGGCACACCGCTGAGGGGGAGGAGCCCCAACGCTCTGCAACGGCGAGATCGC
GGTACTCCAGGCCACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GGCACAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCTGCGCCGCCCCGG
GCCGCTTAACCTGAGCTATGCCGCCCTTCACTGCAACGCCGGCTCTGGACTCAG
TCCACCTGGGAGGGAGGTGAGCTGCGCTGCCGGGAGCAGCTCCGATCTCAGTTACTGCA
TCGGCGACGAATCGGCCTGCTGGGACAAACTCTGGCGATGTGTTGTGCTCCCTGCCCC
GGGAGGTACCTCCCTGCTGGGAAATGCGCAGAGCTCCCTAACTGCCCTAGACGGACTTGGGAGG
CTTGGCCTGCAATGTGCTACGGGCTTCAGCTGGGAGCTGGGAGGACGGCCGCTTGTGACCA
GTGGGGAGGACAGCGGACCCCTGGGGGAGGGGGGGGGGGGGGGGGGGGGGG
GCAACACAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGAGGAGAAGCTGGGAGAGAC
ACCACTGTGCTGCAACAGAACATTAACATCTTCTGAGATTCCTGAGATTCCTGAGGGAT
CACAGAGCACGATGCTCACCTTCAAAATGCTCCCTCAAGGGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCCAAGTTAATCTACGACTCTCTGCCACTCTCAGGCTT
CGACTCTCCCTGCCGTGTTCTCATATTGTGAGCACAGCAGTAGTGTGAGTCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTGTGCTTCACGAACGCCCTTCCCACCA
AGGAAGGAGTCTATGGGCCCCGGGCTGGAGAGTGTCTGAGGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCAAAACAATGGGTGAAAGTGGGCTGTGATCTGGGGAGAG
CAGAGGGTGCCTGGCAGGTGCCCCCTTGGCTCTAGTGTGATGCA**TAGGAAACAGGGGA**
CATGGGCACTCTGTGAACAGTTTCACTTTGATGAAAGGGGAACCAAGAGGAACCTTAC
TTGTGTAACTGACAATTCTGCAAGAACATCCCCCTTCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCAACTCTTCCCTGATGATAGAGGAAGTGGGAAAGTGGCTTAA
TGCTGATACTGGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTCTATGTTTATTGGAGAA
TTGGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACAAAATGAAAGGAAATGTTCTATGTTGTTCAAGCTAGGAGTAT
ATTGGTTCGAATCCCAGGGAAAAAATAAAAATAAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVIALLLRAGPGGGGSKLLFWVALEERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCSTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFLHSAALDFSPPGTEVSALCRGQLPISVTCAIDEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVIFIVFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSAHCTNNGVKGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCACCTCTCAGGGAAACTAAG
CGTCGACTCAGCGGCCAACATAATCGCCTTAAAAGTCGCCTCTCCGGCGCGCTATC
CCCCGGCTACCTGGGCCCGCCCGGCCGGCTGCCGGCTGAGAGGGGCCGGCGCAGCGGA
GCCGGCTGTGAGCCAGCCTGCTGCCAGTGTGAGCGGGCGGTGTAGCGCGGTGGCGG
GGGGCGTGTGCGCGCCGCCGTGGGTGCAAAACCCGAGCGTCTACGCTGCGCATGA
GGGGCGAACAGCGTGGGCCAACACTGGCTGTGGCTGCCGCCACCCAGCTCTCGGG
CAGCAGTCCCAGAGAACCTGTTCATGTTCACTATGGTGGCATTCTTACTGGAGACTGTGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCTCCAAATAGCAAATGACTTGGAAAATCA
CACTTCCGAAAGGAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAAC
CTGTGCGCATGAACTGACTTTGGATGTGTAATGGCCATGCCGCAATGGCCGCGCATGG
CTTCTGGCACTTCCGGCTGGACCCCTGGTGTGCACTGGCAACAAAGATGTTGGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGACTCTTGCACAGACCTTCGGCCTTTAAACAA
CCCCAACTGGCCAGACGGGATTAACCTCTGGAGACTCTTGTGTTGGCACAATTGTAGCC
CAAAGAACATGCCATTAGAATTAAAGTTGAGAAGTTGATGTGAGGCGAGATAACTCTGC
CGATATGATTATGTGGCTGTGTTAATGGGGGAGTCACAGATGCTAGAGAAATTGGAAA
GTATTGTGGTGTAGTCACCTGGCCCAATTGTGTGAGGAAATGAACTCTTACTTGTAG
TTTATCAGACTTAAGTTAACTCGCATGGCTTATTGGTCACATACATTAGGCCAAAA
AAACTGCCAACACTACAGAACAGCCTGTCACCACACATTCTGTAAACCACGGGTTAAA
ACCCACCGGGCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGTACTTGTATTAGCCGGCATGTTATCACAACCATCCTCGCAGTGGAGGT
CACGCCAACATCTGGCATCACAAACTCATCAGGGGAAATTCTGGCATTGAGCGGG
CAAGAACATGAGTGCAGGCTGACTGTCGCTGCAAGCAGTGCCTCTCCTCAGAAGAGGT
TAAATTACATTATTAGGCCAACAGTAGGTTGAGAGTGGCGAGGAAATCTGCCAACAGC
TTTATCATGATGTTCAAGGACAAGAATCAGAGACTCTGGATGCCATTAAAAAAAGAACATG
TAAACAGTGAACGTGTCCATTAGCTGTTACTCTGGCATTGCTTGTAAAGATCTATGTC
TCTCAGTAGAAAAAAATACTTATAAAATTACATATCTGAAAGAGGATTCCGAAAGATGG
GACTGGTGTACTCTCACATGAGGGATGAGGCTCCGGAGATGCTGGAGGAGAATGTC
TCTGGCTGTGAGAGGAGCAGCTATGTTGGCAACCTGGCAGACTTGTGCGTGTAGAG
AGCTAAAGTGTCAAGCGTTGACAGCTGGAGAGCTTATTTATACATCTGTAAAGGAT
ATTTTAGATTGAGTTGTGAGAGATGCAAAAGGATTAGGATGCAATATTAGT
GTTATTGTTCCACCTTCAAGCCCTTGGCCTGGAGGTGTTACATCTGCTTGTGCGTT
ATCATGCTTAAATAATTAGTTAAAGGAAAAAAAG

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVPNNGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTIITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACCGGTGGCGGACCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCTACGAGGTCCCCAGCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTCTGGGCTCACGCTCTTCTCAACCTCCAGAACCTATCTGG
CTCCAGGCTCTCACCCCCAGTCTTCTCCCCGCTCACGCCCACCGTGTACACCTG
CCGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACATCGGGACAACCTGGAG
GTGGAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCCTGGTGGTTTACAAGCAGCAGGAGGCCGGACCTTCTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAACAGAGGGCCCTGGGTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTCCAAGCGGCTACGGGGTGAGGCTGTGGCC
AGTGTGGCCTGGCTACTTGAAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTGGCCCTGTGCCGATGCTCACCTGAAGTGTGAGACATTGATGAGTGTGGCACAGAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCGCGCTAGGTGCTGGGGCAGGGCAGGTGCTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGCTTCAAGTGTCTCGATGTTGAGTGTGAGACAGAGGGTGTCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGTACAAGCAG
ATGGAAGGCATGTGTGAAGGGCAGATCCAGACTCAGCAGGCTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCACTGGATGAGTGTGAGACAGAGGGTGTCGGGAGAGA
CGCTGGCTGCTAAGGGCACTGGTGTGCTGGCATCTGTGCCACTGGCA
ACTGGCTACTGGTGTGAGAGCAGTGCAGGGCTTCATCAAGGGCAGA
ATCGCGGCCACCCACCTGTAGGACCTCCCTCCACCGCTGCCAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAGACACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCACTGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCCTACAGGGGTGGGCCATCACAGCTCCCTGCACTGCTGCA
TCTGTGTTGCTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLESELVESWWFHQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGCQCEGEGTRGGSGHCDQCAG
YGEACQCQCLGYFEAERNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA
GCACC**ATG**CAGCCCTGTGGCTCTGCCACTCTGGGTGTTGCCCTGGCCAGCCCCGG
GCCGCCCTGACCGGGGAGCAGCTCTGGCAGCCTGCTGCCAGCTCAAAGAGGT
GCCCACCCGGACAGGGCCGACATGGAGGGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCACGGGACCGCTCCCGGGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTGGAGGCCAGCACACACTGCTGGTGGCG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGCTGCCAGGCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCAGGCCACGGGCGCTGTCCCCCGCGAGGCCGGGCC
CGGGTGACCGTCAGTGGCTGCCGCTCCGCCAGCACGGCTCCAACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGTCAAGAGAGCGCTGGAAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGCAGCAGCTGAGCCGGCCCGGAGCCGCTGCTCACAGGTGTCGGTCAAGAG
GAGCATCTGGGCCGCTGGCTCCGGCAGCCCACAAGCTGGTCCGCTTGCTCGCAGGGGC
GCCAGCCGGCTTGGGAGCCCGAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCATAAGCAGGCCGACCCGCTGCTGCCGCCAGGAG
ATGTAATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGTCGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGGCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCAAGTGGTCAGCTGCCAACATGAGGGTGAGAA
GTGCACTGTGCCCTGGATGGTGCCTGCAAGGAGGCTCCAGCCAT**AGGCGCTAGTG**
TAGCCATCGAGGGACTTGACTGTGTCAGCTGAGGACTACCGAGAGCTG
GGCATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTACCTCACCTAATTGGCTCTCAGGAATGAGAAATTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCTGTCATTGTTACTTGCTGTCAC
TGGATCTGGCTAAAGTCCCTCACCACACTGGACCTAACGACCTGGGTTAAGTGGGT
TGTGCACTCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPHRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP
VPKAALHRHGRSLSPRSARARVTVEWLVRDDGSNRRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRRPQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEQPLLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFWKPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCTGAGAATAACCT
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTCTCCCCTGTTGAGTGGAAAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAAAACAAGATCACAGCTCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATGT
GCTTGTCCTCCATCCAAGCCTACAGTTAACATCCCTCTGCCACCATGGGAACCGGG
CAGTGTGACATGTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGATGCCATCGAACCTAAAAGCACCGTGCCTCAGCAACTCTCTATGCTCT
GAATCCCACAAACAGGAGAGCTGGCTTTGATCCCCCTGTCAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACCGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGGAGCGGAATGTGGGGGTATCGTGGCAGCCGTCCTGTAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCTATAGCGAGGCCACTTGACAGAACAAAGAACGGGA
CTTCGAGTAAGAAGGTGATTACAGCCACCTAGTGCCTGAAGTGAGGAGAACAAACAG
ACCTCGTCACTCTGGTGACCTGGTGCCTCACCGCCTATCATCTGCACTTGCCTTA
CAGGTGTACCGGACTCTGGCCCTGATGTCGTGAGTTACAGGATGCCATTGCTTC
TACACCCCACAGGGCCCCCTACTCTCGGATGTTTAATAATGTCAGCTATGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGAGGAATCTGCACTCACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTCTGTA
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTGGGCCACTCTTCTGCTTCCATGGGAAGTG
CCACTGGGATCCCTGCCCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAATGGGAGCTTGTGAGGAGCATAGTAATTTCAGAGAACCTGAAGCCAAAG
GATTAAAACCGCTGCTAAAGAAAAGAAAAGTGGAGGCTGGCGCAGTGGCTCAGCCTG
TAATCCCAGGGCTGAGGCAGGGCAGGATCACCTGAGGTGAGGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTCATGCCCTGAGTC
CCAGCTGTCAGGAGGCCTGGCAACAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 44

MGTTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCTMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
CGCTGGCGAACAGGGGCTCTGGGCCCTGGCGCTGCTGCTGCTCGCTCGGACTAGGCCT
GGAGGCCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTAGCAG
GCTCGTGCACCCCACCAAGTCCAGTGCACGCCAGTGCTTATGCGTGCCCCCTACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCTCCCTGCCCTGCACCGGGCTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGGCCCTGGCTGCCTAGCA
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCAGGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAAACCAATGAGATCCTCCCGAAG
GGGATGCCAACCATGGGCCCCCTGTGACCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGAAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCCGACCCCTCCCTTGTGCTGGCTCCGAGGCCAGGAGCGC
CTCCGCCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCCTGAGACAAGCATTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGGATGGTACCCGGCACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAGAAAGTGGCCCTGGAGATTGAGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTC

FIGURE 46

MGGWMAQVGAWRTGALGLLLLLGLGLEAAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLCSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRLAACLAGELRCTLSDDCIPLTWRCGDGHPCPDSSDELGCGTNEILPEGDATTMGPV
LESVTSLRNATTMGPVTLESVPVGNAATSSAGDQSGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSPL

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACACGCGTCCGGTCTCGCTCGCTCGCGCACGGCGGAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAAACCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGTT
CGATGACCTCAAGTGTGTGCTGACCCGGATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCCATTCACTGCCAACAGCGATTCAAGCTGAAG
GGCGTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAACTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTAAATCGAAGATGCTGAGATTCAA
ACAAGACATATAGACATGGAGAGAAGCTAACTCATCACTTGTATGAAGGATTCAAGATCCG
TACCCCGACCTACAAATATGGTTCAATTGTGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTCCCGGTTGGGACTGTGATCTCTATCGCTGCTTCCGGATTAAACCTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAACTCTGTCACACTCCAATGGTAGTCACTGGAGATTCTCT
GCCACCCCGCCCTTGTGAGCGCTACAACCAAGGAACTGTGGTGGAGTTTACTGCGATCCT
GGTACAGCCTACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCT
TTATCAAGTCTACTGCATCAAATCAGAGCAACAGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTGGTAGACGGCGTGGCGTCACTGCTCCGTCATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTAGGCCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACAGGA
CACAGGCCAGGGAGTCAGAAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA
GTCTGTATTCAACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCCCTGACATA
ATTGCCAGCAGGCCAGAGGAGGTGGCATCCACCAAGGCCAGGATCCATGCCCCACTGGT
GTTGTTCTAAGAAACTGATTGATTAAGGAAATTCCAAAGTGTCTGAAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTCTCTTGGTTTAGACAAATGTAACAA
AGCTGATCCTAAATGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTCTGACACAGACTGATTTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKAGTKRLCLKHFNGLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSPVGTVISYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYITCQYGEWFPSYQVYC1KSEQT
WPSTHETLLTTWKVAFTATSVLLVLLVILARMFQTKFAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCGGCCCTCCCCCGCTCCCGTGCCTCGGTGGCTAGAGA
TGCTGCTGCCGGTTGCAGTTGTCGCGACGCCCTGCCGCCAGCCGCTCACCAGCGT
AGCGCCGAGTGTGGGGGGCGCACCGAGTCGGGCCATGAGGCGGAAACCGCGTACAGG
CCGTGCTGCCGTGCTGGTGGCTGCCGCCAGGGCTGCCGCCAGGGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCTTGA
TAAAGTCATTACTCCATGATACTCTCGAAGACTGAACATTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAA
CTGATAGAAAGTTCATGAAAACCTCTGCCATCTGATGGTGACTCTGGATTGGCTCAGGAGGCGTGA
GGAGAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGACTGATGGCAGCATAT
ACAATTTAGGAACCTGGTATGGATGAGCGCTCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCCACCGCTGGCATCGAGGCCCTACATGTTCACTGGAAATGATGA
CCGGTGCAACATGAAGAACATTTCATTGCAAATATTCTGATGAGAACACAGCAGTCCCT
CTAGAGAACGCTGAAGGTGAGGAAACAGAGCTGACAACACTGTACTTCAGAACACAG
GAAGAACGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCTCTCCCTCTTGTCGGTACCAAGCTGTATGTTGGTT
GGATCTGTAGAAAAGAAAACGGGAGCAGCAGACCCCTAGCACAAGAACACACCAC
TGGCCCTCTCCTACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAA
AACGCAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCACTCCAGTGT
CGGGAGAACGCACTCCCGATGACATGCTTGACTATGACAACATGGCTGTGACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGCTGAGCTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGCTGGATGGTGGAAAATGAAATATG
GTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAAACAAGCTTAGATCAGGCTCTGT
GGATGAGCATGTTCCCCAGACCTCTGGTGGACCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGCCACCTTATGAGAACGGTACCTGCCAGGTCTGCCACATAGTA
GAGTCTCAATAATGTCACCTGGTGGTTGATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGTAAAGATGGGCTGGAGCTGGAAAACCACCTCTGTTCTTGCTCTACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAGGCCACATATGGTAGCACAG
GTTGGCCTGTGACCGCAATTCTCATATCTGTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NPFEEAKEACRRDGGQLVSIESEDEQKLIEKFIEENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAGEETELTPVLPTEETQEDAKKTFKESREAALNLAYILIPSIPLLLL
VTIVVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGTCTCCCTCAGGCCGGAGGCACAGCGTCCCTGCTGCTGAAGGGCTGGATGACGC
ATCCGCAGGTTCCCGGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCAGGGCCTACCACATGATCACTGGTGT
GTCAGCATGCCCTGTGGACCCCAGTGGCGTCCCTGACCTCGCTGGCTACTGCCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCGGTCGACCCGCAGC
CTGCTGAAGTTGAAAATGGTCAGGTGCTGTTCGACACGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCAACCTGAAGGGGGCATGTTTGTGGCAGTGACCAAGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGTCTTATTGTTTCACTAACATTTCGGATCTG
GAGTCCACCCGGTTGGCTGGCTGGCTTTCCAGTGTCAAGAAAAGAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTGTATCCAAACTACCAAAGCTGCTGGAGCCCTGA
GGCAGAGAACCAAGGGCGGAGGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGAACGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTTCATCTCCT
GGACAACGTGGCTCCGAGCAGGCACACAAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTCAGATGGCAGTAGGCCATTCTCCACATCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTAAATGACCCCTGGGATTGGTACACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACATTACAGCACCTGAATCTAAGGAGTGGTTGTGAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFPNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRRRQTAISLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAA
ACTAAATTTGCTGCTGGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCCTGATCCTT
GCCATTGACCAGACCTGGATTCTAGCGCTCCATCTGGAGTGCAGCTGGCTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGAGGTGAAACAGAAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTGCGGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCCTAGTGGTATTITGTATGAGGCCACAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGGCTCTTCTCCCCA
GTCCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGGTGGAAAGTGA
GCACCAAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCGGGCCGAAAGGTGG
TGTGCCGCAGCTGGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAACCCCTTCA
GGATTGCCCTTCTGGGCTTGGGGAGAACACCTGCAACCATGATGAAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGGAGACAAACCTGCTCTGGGCACTG
GAGGTGCTGCACAAAGGGCGTATGGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGGTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGGAGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTATGCTCAGTGTAGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCATGACTGCATGGGATGAAACACTGATCT
TCTCTGCCCTGGACTGGACTTAACTTGGTGCCTGCTGATTCAGGCCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTAGGCCATCAGACATAGTTGAAACTACATCA
CCACCTTCCTATGTCCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTTGAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACAC
CACCACTTGTCTGTTCTCTGAAGAACCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACCGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPCHCKGRVEVKHQNWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGGTCTATCGATTGAATTCCCCGGGGATCCCTCTAGAGATCCCTGACCTCGAC
CCACGCGTCCGGGACCGTGGCGGACCGGTGGGCCGCTACCAGGAAGAGTCGCGGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGGCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCACCTGCGGAATGCTG
TGGTGGTATCACAGGCGCACCTCAGGGCTGGCAAAGAAATGTGCAAAGAGCTCATCAGAGA
GCGGGTGTAAACTGGTGCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TCCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATTCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGAA
CTGTCTGCGTGGCAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACACCCACAGGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTCTCAGCCTCATGGCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCAGCAGTCTTAGGTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGTCTCACAAGTGG
AAAGACTGAAGAAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAAATATGGAGCTGGGTTAACACT
AAAAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAGGGCGGCGCGACTCTAG
AGTCGACCTGCAGAAGCTGGCCGCCATGGCCCAACTTGTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTAKLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAAGVV
YTSDLFLATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVINGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCGGCGGACCGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGACACCGACTGC CGCACCTGAGAGATGGTGGTGCCTGTGGCTTCTCCCTACAGAAGT
TTTCGCTGGTCTGTGATGCCCTGGCCCTGTGATGGGCTGTTCTGCTCCCTACAGAAGT
GTTTCATGCCACCTAACGGAGACTCAGGACGCCATTATTCACCCCTTACATTAAGC
TGGGAAGATCCAAAAAAGGAAGAGAATTGAGATTTGGCTGGCCCTTCCCAGGACTGAAACATGA
AGAGTTATGCCGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTTCTCTGGTTC
TTCCAGCTCAGATAAGCCAGAAGATGCCAGTAGTTCTCTGGTACAGGGTGGCCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTCACAAGTAAACATGA
CCTTGCCTGACAGAGACTCCCTGGACCACACGCTCTCATGCTTACATTGACATTC
GTGGGCACAGGCTTCAGTTACTGATGATAACCCAGGATATGCAGTCATGAGGACGATGT
AGCACGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCAGTGGGAGCTTATGAGGGAAATATGAGGACCCATTGACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGGTTGAAGATCAAACCTGAAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGAGAATTCCCTGTACCAAATTGGCT
TGTGGATGAGAAGAAAAAAAGTACTTCCAGAAGCAGTCCATGAATGCAAGAACACATC
AGGAAGCAGAACACTGGTTGGGCTTGAATACTGGATAAAACTACTAGATGGCAGCTTAAC
AAGTGTCTTCTACTTCCAGAATGTTACAGGATGTAATTACTATAACTTTGGCT
GCACGGAACTGAGGATCAGCTTACTATGTAAGGAAATTGGTCACTCCAGAGGTGAGACAA
GCACATCCACGGGGAAATCAAGCTTAACTGAGGAAATGAGTGGAACTATAGTTGAAAAGTACTTGGCAGA
AGATAACAGTACAGTCAGTTAACCTGGTTACTGAAATCATGAAATAATTATAAGGTCTGA
TCTACAATGGCCAAGTGGACATCATGTCGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGGAAGGAGATCCCGAAATACAAGAAGGAGAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCCGCAAGCGGGTGA CTTCCATCAGGAATTATT
GAGGTGGAGGACATATTTACCCATGACCCAGCCTCTGAGAGCTTTGACATGATTATCGA
TTCACTTATGGAAAAGGATGGATCCTATGTTGGATTAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATGCAAGATTTCATCAAAATAATTATCCTTGAAAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGGATGAAAGCTATGGATGATGTAACACTGAGACAAAGATGTATAATGA
AATTGGGTCTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTGGCATGCCGTGAAGGT
GTTGGAATATTATGGATAAGAATAGCTCAATTATCCAAATAAATGGATGAAGCTATAA
TAGTTTGAAAAGATTCTCAAATGTTAAAGTCTTAGAACAAGAAATTCTTGAAATA
AAAATATTATATAAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPFPGLNMKSAYAGFLTVNKTYNSNLFFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPyVVVTsnMTLDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPNVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPYFQNVTG
CSNYYNFRLRCTEPEDQLYYVKFLSLPEVRQAIHVGQNQTFDNGTIVEKYLRDVTQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWDPPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCGGCTCGGAATGGCACATGTTGGGATCCCACTTGTGGCTACAAACAT
TTTCCCCTTCTAACAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGT GACCAGCTCTT
CCTCTGTGATAACAGAGCATGAGAAAAGTGAGAGATGCAAGGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTCAGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGGAGAGC
CTGGGGAGGGCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGGTTAGTCTTAACATTGAGTGGCTTAAGGGCCAGAAA
TGAACCTCAACAGCCTTTAACCTCTGTGGAGATGAAAACGATGGCTTAAGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTTAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCTGAAACATTCTAACAGGGAGAAGTATGTTAAAATA
GAAAAACCAAATGCGAAGGAGGAGACTCACAGAGTCAACCAGGAT**T**GGGACCTGGGTC
AGGCCAGCCTTGTCTCCGGAAATTATTTGGTCTGACCACTCTGCCCTTGT
GCAGAACATGTGAGGGCCAACGGGGAAAGCTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGG CAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCGCTCTGTGGCTCTGCTCAGTGTGGCTGGGTGCTGGCCCCCCAGCAGGCCGC
ATGCCCTAGTCAGCACCTTCACTTGAGAACATGCTGACCTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGCTATGTGGGGCCATACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCAGGTGGCTCATAAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTACCCG
CCCCCATCGTGAGGGCTGAGGGCTCACCCCTACCAAAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACAGGCCCTGGCTGTGGAGCCCTACCAAGGGGCTGTCA
AGCTGCTGGGTGGATGACCTCTTCATCTGGTGGAGGCATCCCAAGAAGGAGCACTAC
CTGTCAGTGTCAAAAGACGGGACCATGACGGGGTGAATTGTGGCTCTGAGGGTGAGGA
TGCGAACGCTCTCATCGCAGCGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGGAT
TTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCTGGTCTCCACCTTGACAT
CTCTACATCTACGGCTTGTAGTGGGGCTTGTACTTCTACTGTCCAGGCCGAGA
CCCCCTGAGGGTGTGCCCATCACTCCGTGGAGACCTCTTACACCTCAGCATGTGCG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGCTGACCCGGG
CGGGGTGGAATACCGCCTCTCAGGCTTGCTACCTGGGCAAGCCTGGGACTCACTGGCC
AGGGCTTCAATATCACCAGGCCAGACGATGACTACTTGTGGCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCATCGGGCATCAACTT
GCAGATCAAGGGAGCCCTGAGTCCACTGGAGGGCAACCTGGAGCTCAACTGGC
TGTGGGGAGGACGCTTCACTGGAGGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACAC
CAGCAGGGACCGCATGACCTCTGTGGCTCTACGTTACAACGGCTACAGCTGGTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAAGTGTCCAATGCC
ATTCACTTCTCAGCAAAGAGTCCCTCTGGAGGTAGCTATTGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAAACAAAGG**T**GAATGGGAGGTAGAAGGGGTTATTTGTG
ACTTAGCTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCTAACCTTAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPGNWFWSDHSAACFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSSRVVLLSVVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGTGNLTIQVAHKTPGEEDNKSRYPPLIVQPCSEVLTLNNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPKHKEHYLSSVNKTGTMGYVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFAASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFIAIFSKGQKQYHHPPDDSAACFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTCGGACTGGAGTGGGAACCCGGGCCCCGGCTTCTGGCTTGAGAACACCGCATGACCA
CGTGGACGCCCTCGGGGAGGCCGGCAGCTGGACTCTCTGCTGTCTTGGGCTTCCTGTGCTCC
GCAGGGCTGGACTGGAGCACCTCTGGCTCCCTCTGGCTCCGCCATGCACAGCTGGGCTGAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCTACATTTCTGGCTGCCCCAGGGAGTACT
GGAGGGACGCCCTGAAGATGAAGGCTTGAGCTTGAACACCCTCAACCTATGTCCTGGAAACCTTCATG
AGCCAGAAAGGGCAAATTGACTCTCTGGGAACTGGGACCTTGAGGAGGGCTTGCTCTGATGGCCGAGAGATCG
GGCTGTGGGTATTCTGCTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCCCAGCTGGCTAC
TCCAAGAACCTGGCATGAGGCTGAGGACAACTAACAGGCTTCAAGCGTGGGGACCTATCATGCGCTGAGGAGAATATG
TGATGTCAGGGTGGTGCACCTCCAGTCAGACGCTGGGAGACTTCAAGCGTGGGAGACTTCAACTTGCAG
GTTCCTATAATAAAAGACCCCACATACATGCTCCAGCTCAAGAGGACTCTGGAGACGGTGCATGTGAACCTGC
TCTGGACTTCAAGGACAAACAGGATGGCTGAGCAAGGGGATTCTGGGAGGACTTTCAGGCAACATCAACTTGCAGT
CAACACAGCTGAGCTGAGCTTCAAGGCTTCTCTTCAACGTCAGGGACTCAGCCAAAGATGGTATGGAGT
ACTTGAGGGGGTTGTTGACTCTGGGAGGCCCTACAAATATCTTCTGGAGGTTTGAAAACCGTGT
CTGGCATTCAGGCTCCATGACTACAAGTCAGATGTCACAGCTGACTGATGATGCTGTGAGAGGCCGG
ATTACAGGCCAACATACATGAGGCTCTGGCAGACTTCTGGGCTCATCTGGGAGGAGGAAATGGAGAATATG
ACCTCTCCCCAAAGTACCTGGGCTTAAACCCGCTTCTGGTACCTGTCCTGTGGGAGCCCTCAAGTAC
TGGGGAGGCAATCAAGTCTGAAAGACCCATCAACATGGAGAACCTGGCAGTCAATGGGGAAATGGACAGTCT
TCGGGATCACATTCTGAGAACAGCATCACCTCTGGCATCTGGGAGCCACTGGCATGATGGGGAG
TGTGAGAACAGTATCCATAGGATTCTGGACTACAAGAACAGAAGATTGCTGTCCTCTGATGCCAGGGT
ACACCGTGTGAGGATCTGGTGGGAATCTGGGGAGACTGAGGAACTGGGAGGAAATTTGATGACCCGGCAAG
GCTTAATTGAAAATCTTCTATCTGATGATTGACCTCCCTTAAACCTTCAGAACATTTGATGAGGAAAG
GCTTCTTCTGAGGGCTCTGGGCTCATGGGAAATGGNNTCTCTCCCTGGGAAACACCCACATTACCTGCTTCTCTGG
TGAATCTGTCATGAGCTCCAGCCTGGTGCACCTTCTGGTACGAGGCTGGGGCTGGGAGAAGGGGGTTGATTCA
TCATGAGGGAGGAACTTGGAGGTTCTGGGACATTTGGGACCCCCAGAAGAGGCTTACCTCCAGGCTTGTG
GCCGGGAAATCAACAGGTCTGGTTTGGAGGAGGATGGGGGGCTTGCTTACAGTCAAGGAAACCCCC
ACCTGGGCAAGAACACTAACAGTCTGGGCTGGGCTGGGCTTACCTGGGAGGACTTGCAAGGAAACCCCC
CTCTTGACTGAGGCTTGGCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG
ACTGGGGGGTACAGTCTGGCCCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG
TGCTTCTGTTGATGATGCTTCTAGGCCCTGCTTGTGCGAGGGCTGCTGGGCTGCTCTAGGGGGTGGCTGGGAGC
AGCTAATCAGATGCCAGGCTTGGCCCTAGAAAAGTGCTGAAAGCTGGCCCTTGACGGGAGCTGCAAGGCC
TGCGAGCATCTGGTGGACTCAGGGCTGCTTCTGGGAGGCTGGCCACATCCCTCATGGGGCCAT
TTATCCCCAAATCTCTGGGTGTCACAGTGTAGAGGGTGGGGAGGGGTGCTCTCACCTGAGCTGACTTTGTT
CTTCTCTTCAACTCGCTCTGGGCTTCCACAGGGTGACAGCTGGGCTGGGAGAACAGAAATCTCACCTGCTTCC
CAAGTTAGCAGGTGTCCTGGTGTCTGAGGAGGACATGTGAGTCTGGCAGAGGCCATGGCCCATGTCATGCA
CATCCAGGGAGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACAGGCCATGGCCCATGTCATGCA
AGGGAGGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACAGGCCATGGCCCATGTCATGCA
GAAGGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACAGGCCATGGCCCATGTCATGCA
GAAGGTGTCAGTGGCATTGAGGCTTGTGAGGCTTGTGGGGCCAGGCCACACTGGCTGGGCTACTGCTG
GTTGAGTAAAGCTATAACCTTGAATCACA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTTTYVPWNLHPERGKFDFSGNLDLEAFVLM
AEIGLWVILRPGPYICSEMDLGGLPFWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMRSVVPLQ
YKRGGPPIAVQVENEYGSYNKDPAAYMPYVKKALEDRGIVELLTSNDKGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGWFDSWGGPHNILDSSEVLKTVAIVDAGS
SINLYMFHGGBTNFGMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDPLLKPMPYEPLTPVLYSLWDALKYLGEPIKSEKPINMENLPVNNGNGQSFGYILYE
TSITSSGILSGHVHDRVQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRLVENRGRVNYGEN
IDDQRKGTLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLYSIS
STPCDTFLKLEGWEKGVVFINQNLGRYWNIGPQKTLYLPGPWLSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGGAGCTGAGGGCTCGGGCTAGCTAGGTGTAGGGTGGACGGGTCGGAGACC
CTGGTGAGGTTCTACTTGGCTTCGGGGTCAAGACGCAGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTGGCCGAGGCCCCCAGGACCTCATCTCCCATGTTGGAGGAATC
CGACACGTGACGGTCTGGCCGCTCAAGACTAGAGGAGCCTGAAACGCCATGGCTCCC
AAGAACGCTGCTCGTCTGGCTGAGGGTCAAGCGCTACTGCTGCCCA
GGCAGACACTCGGTGTTGTAAGGGTCAAGCGCTACTGCTGCCCA
CGTTCCGCTATGTGCTGGCAGCGTCAACTACTTCTGGTACCGCGGTGTTGGGCCAC
CGGCTTGTGAAGATGGCATGGACGGCCATAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCTGGGTCTATAACTTAACTGGCAGGGGACCTCATTGCTTCTGA
ATGAGGAGCTGAGCTGAGCAACTGTTGGTCAACTGAGAACAGGACCTTACATCTGTGCAAG
TGGGAGATGGGGGTCCTCCATCTGGTGTCTCGAAACTGAAATTCTACATCTAACGAACTC
AGATCCAGACTCCCTGGCGAGTGGACTCTGGTCAAGGTCTGGCCAAAGTATATC
CATGGCTTATCATCAATGGGCCAACATCATTAGCATTGGTGGAAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTTCTGTGACTGCTAGG
AGAAAAGATCTGGCTTCAACACAGATGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GACTCTTACACTCTGAGATTCTGGCCACCTGACACATGACCAAAATCTTACCTCTGCTT
CGGAAGTATGAACCCCCTGGCATTGGTAACACTGAGTACTCACAGGCTGGCTGGATT
CTGGGGCCAGAATCACTCCAACCGCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGGCCAGTGTGAACATGTACATGGTCCATGGAGGTACCAACTTGGATATTGG
AAATGGTCCCAGATAAGAAGGGAGCTTCTCCGATTACTACAGCTATGACTATGATGACCC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTTGCTCTTGAGATGTCAAG
TCAGGAAGTCTGGGACCTTACCTCCGGAGCCAAAGATGATGCTGGACCTGTG
ACTCTGACCTGGTGGCATTTACTGGCTTCTCTAGACTCTGGTCTGGCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGGAGGCTGTCAAGCAGGACCATGGCTCATGTTGAC
GAACCTATATGACCCATACCAATTGGTGGAGGCAACACATTCTGGTGCACAAATAATGGAGTC
CATGACCGTGCATGTGATGGTGGAGGGTGTCCAGGGTGGTGGAGCAGGAAATATGAG
AGACAAACATTGGTGGAGGGAAACTGGGCTCAAACATTGGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTGAACGGGCTGTGAAGGCCAACATTCTG
GGCAAAACAACTTCACTGGGAGCTGGATGATGTTCCCTCTGGTGGAGGAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCAGTGGCAAAATGGCCTATCTCAAGCTCTCTGGCCCCACATCT
ACTCCAAAACATTCCAATTGGCTCAGTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCGTACTGGACAAAGCAGGGCC
ACAAACAGACCTCTACGTGCCAGATTCTCTGTTCTAGGGAGGCGCTAACAAAATTAA
CATTGCTGGAAACTGAAGATGTACCTCTCAGGCCAACGTTCTAGGGAGGCGCTAACAAAATTAA
CTCAATAGCACTAGTACTTTCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGGCTCTGAACCAATGGAGTTAACGTGGGCACTGAAAGCTAGGCGGAGGCTGGCTCATGC
CTGTAATCCCACTGGGAGGCTGAGGGGTGGATACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCAACATGGTAAACCCCGTCCACTAAAAAATACAAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAAATCC
AGGAGGCAGGGTGCAGTGAGTGGAGGTTGACCTGCACTCCAGCTGGCTGACAGTGA
GACACTCCATCTAAAAAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGQNHSRSVAVTKGLENMLKLGAJVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVLGPLPPSPKMML
GPVTLHLVGHLAFLDLLCPRGPIHSILPMTEFAVKQDHGFLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLVYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSDTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGCCTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCACACTCTCTGGTTATTCAAGGATACCTTGAGGAATT
CTTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAACGATTT
GCCTTCCTCTTACATGGTAGACCAGTATGACCAGCTATACTTCAAGCGTTGGTGT
CTTGTCAAGAAGTTAGTGAAGAAATTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCAACGCCAGGACAAGCAGGAGTTGATCTGTTCATG
CTGTCGGGGGTGCGCGATGCTGCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGACT
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCTGGGTGTATTGCTAAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCAATTCTAAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCAATTACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTCTCTAACACAAAGCTGAATCCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTAACACAACTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGAACAAAGTGGACATTCTGC
AAAAACAATTGTTAAATGCTAAAGTTGAGGACTTTGATCTGGACAGAACATGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACCTG
CTTGGACCGCTGCCAGCCAGCTGGGAGCTGTCGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAAGATCACCTTTTGATACCTGCCACTCGAAGTCAGGACTTGAATCAAGACATA
AAATTCCCTTGCCTAAAGGGATTTAAACTAAGATAATATGACAGTGTGAGAAC
AACTTCCCTAGATTGCAAGTGCCTCACGTACAAGTTTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAGTCATTCAATTCTCAAATCATTTTTTTCTTTGGGG
AAAGGGAAAGGAAAATTATAACTAAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAATTGCTGCCGCTCAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAA

FIGURE 68

MAIMMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRFGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDSLTDLVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMGLESRLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTLKLVLVNSLKKMMNVAELELQNCELERIPHAFSLSNLQELDLKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGONCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCGGGCTTCTCTGGACTTGCAATTCCATTCTTCTAGGACAAACTGACTTTTTATTC
TTTTTCCATCTGGCCAGCTGGATCCTAGGCCCTGGAAAGACATTGTGTTTACACATAAAGGAT
CTGCTGGTTGGGGTTCTCTGGCTCCCTGCATCTGGCATTTGCTTGTGTTGGGGAGGGAGACAGCTGG
GCTCAGTGTGCTGACTTATCTGCTTAGGTACATCGAAGTCTTGTGACCTCATACAGTGAATTGCTGTC
ATCGCTGGTGTATCTGGCGGCTTGCTCCCTGCTGATAGTTGTGCTGCTGTCTTAACTCAAAAC
GCCCTAAAGCTGCAAGGAACCTGAAAGCTGTGGCTGGGACATAATAGGGCTCCCTGAGTTAGGAAAGGCTCCCTTC
AAAGCAGGCCCTGAAGACTCAATGTGTCAATGGCCACCTGTGTTGTGATGTGCAAGGCCACAGAAGGCCAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGAAACAGCTGCTGGAGATCCTACAGAGACTTC
CACTGGGGGCAACCCAGGAAGGAGTTGGGGAGAGAACCCCTACTGTGGGAAATGCTGATAAACACAGCTCA
CACAGCTGCTCATTCACAAACATCACCCCTTGCGCTGGCAACTGACCTTCCCCTGGAGGTGTC
GGTGTGATTAACACAGAGCTTGCGGTCTTAAGGCTGCCAGGCCCTGGCAAATAATGGAGCTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTCTGTTTGGCGAGGCTGACAATGGCGAGGCTGAA
GCAAGCTGCAGCTCAGTCTAGGGGTTGCAATATGCGAGAGACCAAAAGGCTGACAATCTGCAACTCAATCCC
AGTGAGAACTGCACTGGACAAATGAGAAAGCAGGAAACAAAGGCTGACAATTATCTTCTGTCAGCT
GATCAGATGGAAACTGTGAGAAGTGAACCATTCAGTGTGATCATCATCAGTGTGACATTGAGCTTCAAAATGTTACT
GACTCTGCAAGAAATCAAAAGACTGTCTTGTCTCTACTATTCTCTCTCAACATCTTATTC
GGCGGTGTTACCTGGATACCTTGGAGGATCCTCACAGCCCCAATTACCCAAAGGCCATCCTGAGCTGCTTAT
TGTGTGTTGGCACATAAGTGGAGAAAGTACAAGATAAAAGGATCTTAAAGAGATTCTTCTGAAATAGAC
AAACAGTGCAGAAATTGTGATTCTCTGGCCATCTATGATGTCGGCCCTCCACCAACTCTGGCTGATGGACAAGTCTG
GGCGGTGACTCCACCTGGAGATCTGTCATCAACTCTGACTCTGCTGTTGCTACAGATTATGCA
TACCGGGGATTTCCTGCTTCTCACCTGCAATTATGCGAAAACATCACACACTACATCTTAACTTGCTCTTCT
GACAGGATGAGAGTTATAAGCAAACTTCCACCTGAGGCTTTAACTTAAAGGAAATACCTGCAACTAAA
GACCCACTTGCGACCAAAATTATCACCTGAGGCTTTAACTTAAAGGCTTCTGCTCTTAAATGAGTGTGGTACAACTCAGA
AAAGTGAAGATCAGTCAAATTACTACACCAATAATCACCTTCTGCTCATCTCAACTCTGAGTGTACCC
CGTCAGAAACAAACTCCAGATTATGAGGTGAAATGGGACATAATTCTCAAGTGGAGATAATATACATCA
GAGATGATGTAATCAAAAGTCACCTGGCAAAATAACACAGCATGGCTTCTTGAATC
TTGAAAAGACTATCTGAAATCACCATATTATGAGGTGAAATCCAAACTTCTTGTCAAGTTAGTCTGAC
ACCTCAGATCCAATTGGTGTGTTCTGATACCTGTAGAGGCCCTCCACCTCTGACTTTGCACCTCCAAACC
TAGGACCTAATCAAGAGTGGATGTGAGTGGAGTAACATTGTAAGGTGATCCCTTATTGGACACTATGGAGA
TTCCAGTTAAATGCTTTAAATCTTGGAGAAGTATGAGCTCTGCTGATCTGAGTAAAGTTGATATGTGAT
AGCAGTGCACCAACAGTCTGCTGCAATCAAGGTTGCTCCAGAACAGACAGACATTCTCATATAATGG
AAAACAGATTCCCATATAGGACCCATTGCTGAAAGGGATGCAAGTGCACAGTGGCAATTAGGATTTCAGCAT
AAACACATCGGGAGAAAACCTTCAACAGTGTGCACTGTGTTCTCATGGTTCTAGCTG
AATGTGGTACTGTAGGACAATCACAGTGGAGGATTGTTCTCAGGATGCCAAAGGAAATGCTACCCCTG
GCTCACACATATTATGAAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGATGAAAAAA

FIGURE 70

MELVRRMLPLTLLSCLAELEMMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
EREPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPPLLGVCSKNNDYVPVFESSSTLT
FQIVTDSARIQRTVVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCWHIQV
EKDYKIKLNFKEIFLEIDKQCKPFLAIYDGPSTNSGLIGQVCRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSITCSDDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYMTIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSVYL
QCCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGAC**ATG**CGGCCCGAGAGCTCCCAGGCTCGCTTCCCGTGTGCTGTTGCTGTC
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCCTGCACCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAGTCCGCATCTTCATCCACTG
GGAGGTGTTTCCGTGCCAGCTCGGTACCGAGTGGTCTGGTGTATTGCCAAAAGAAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCTCCCTAGTTCAAATATGAAAGAT
TTTGGACCACTATTTACAGAAAATTTTAATGCCAACAGTGCGAGATATTTCAGGC
CTCTGGTCCAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTCTGGAATCTGGAATGCCATAGATGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGCAACTGACCTCGCTGTTGGACTGTACTATTCCCTTTG
ATGGTTTCATCGCTTCCCTGAGGATGAATCCAGTTCACTCCATAAGCGGAATTCCAG
TTCTCAAGACATTCGGAGGCTCTAGTACTAGTGTGAAACAATCTAGCCTGAGGTTCTGTGG
TCGGATGGTGCAGCAGGGACCCGGATCAATCTAGGACAGCACAGGCTTCTGGCCCTGGT
ATATAATGAAAGGCCAGTCGGGGCACAGTAGTCACCAATGATCCTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGCCTTACCTGCACTGATCCTGTTATAACCCAGGACATCTTGTGCA
CATAATGGAAAACCTGCACTGAACTAGACAACTGTCCTGGGCTATAAGAGGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAGAATTGGTGAAGCAACTTGTAGAGACAGTTCTATG
GAGGAATCTTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGGCAAGTGGGCTCTGGCTAAAGGATCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCCAGAACATGACACTGTACCCAGATGTGTGTTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCTGGCAT
CCAAAGCTTCTGGGGCAACAGAGGTAAACTACTGGGCATGGACAGCCACTTAACTG
GATTCTTGGGAGCAATTGGCATTATGGTGAAGTGCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCCAACTAATGTGATCT**AAAGTGCAGCAGAGTGGCTG**
ATGCTGCAAGTTATGCTAAAGCTAGGAACATCAGGTGTCTATAATTGTGACACATGGAGA
AAGCAATGTAACCTGGATAAGAAAATTGGCAGTTGGCCCTTCCCTTCCACTA
AATTCTTCTTAAATTACCCATGTAACCAATTAACTCTCAGTGCACATTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGTGATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCACTACTAATATGGGGATATTCTGGGAAATGCAATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCTAGATGGCATAGCCTACTACAC
CACCTAATGTGTATGGTATAGACTGGCTCTAGCTACAGACATATAACAGCATGTTACTG
AAATCTGTAAGGCAATAGTAACAGGGTATTGTATATCGAAACATATGAAACATAGAGAAG
GTACAGTAAAATACTGTAACAAATGGTGCACCTGTATAGGGCACTTACACAGGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAAGTGAAGGCTAGGACATTA
TTGAAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTTCTTCTCAATTATAAAATACATAAGTGTACTGTAACTTTACAACAGTTTAATT
TTAAACCTTTGGCTTTGTAAACACTTAGCTAAACATAAAACTCATTGTGAA
ATGTAA

FIGURE 72

MRPQEPLRLAFLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKKFNAQNQADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPLEYLVNNYQPEVLWSGDGGAPDQYWNSTGFLAWLY
NESPVVRTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIQPTLDGTISVVFEERLRQVGWSLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVVAIFLKWPMSGQLFLGHPKAIGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGAGCTCAACATAGT
TCCAGAACCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACAGTGGCCATC
TGAGGTGTTCCCTGGCTCGAAGGGTAGGCACAGATGCCAGGTGCTCAAGCTGGTCTTG
CTTCTCACTTCATCTGGACACAGCAGGCTCTGGTCCAAGGCTCTTGCGTCAGAAGAGCT
TTCCATCAGGTGTCAGCAGAAATTATGGGATCACCCCTTGAGCAAAAGGCGAACAGC
AGCTGAATTTCACAGAACGCTTAAGGAGGCTGTAGGCTGTGGACTAAGTTGGCCGGAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCTATCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAATGGGTGGTG
TCCTGATTGGAAAGGTTCCAGTGAGCGACAGTTGCGACGCTATGGTTACAACACTATCTGAT
ACTTGACTAACCTGTGATTCAGAAATTATCACCAACAGATCCCATATTCAACACTCA
AACATGCAACACAAACAGAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCT
ACTCTACAAATCCTGGCCCTACTACTCTCTGGCTCAGCTTCCACCTTCTATTCCACGG
AGAAAAAAATTGATTGTCAGAACAGATTTTATGGAAACTAGCACCATGTCAGAAC
TGAACCATTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACCGCTCTGGTAGTGTGGCTCTCTCTTGTGCTGAGCTGGCTTGGATTGTTGC
TATGTCAAAAGGTATGTCAGGCTTCCCTTTACAAACAGAATCAGCAGAAGGAATGAT
CGAACCAAAGTGTAAAGGGAGAACGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGTATAAAACCCAGAACAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCATGCC
GCTGAAGTTTAGATGAGCACAGAACATGGAGACACCTGAGGCTGGTTCTTCTATGCTCC
TTACCTGCCAGCTGGGAAATCAAAGGCCAACAGAACAGAACAGTCCACCC
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAAAGGAGATGC
CCTCTCCATTATGTAACCCCTGTCTGGATCTATCTCTACCTCCAAAGCTTCCCACGCC
TTTCTGCTGGCTATGCTCTAAATAATCCTACCTGGAGAACAGGAGTTTGCAAGTGC
GGACCTTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTCTGGCTGTCTGAGGCTAG
TGGGGTGAAGCCAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGAC
CCTCTTCTCAGCTCTGGAGAACACGTAACCTGGCAGCTGGAGATTCTCATAACTTGAG
AGAACAAAAGAATGGCAGAAAAGTTAGCCCCCTGAAAGGCATGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAAGCTAAAATAAAGAACATGAAACAAGGCTGAGGATACGACAGTACACT
GTCAAGGGACTGTAAACACAGACAGGCTAAAGTGTGTTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTCTGTTCTGCTCTACCACTGCTGATATTTC
AGGAAATATCTTACAGTAACAAAATAAAACTCTTAAATTTCTATTTC
GTTACAGAAATGATTACTAAGGAAGTACTCAAGTAATTGTTAAAAGTAATAAATTCA
ACAAACATTGGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATTATTCTCTAAAGTGCACATAGTGAAGCCTATCTGGGAAGCTATTTC
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTTC
ATTCACTTCTCTAAATGGCAACCCATTATAACCTTAAATTTATTAAACATACCTAACAG
TACATTGTTACCTCTATACACAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTCTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTRLLVQGSRLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKVPVSRQF
AAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTAATTGCTCTCGTGTTCGGTCCGCACCTTCACGATGG
CTCGCCCAACCTTAACCTCTGTCGGCCCTGCTCTCTGCTGCCCTACTCGTAGGGAA
ACTGCGCCTGCTGCCACGGTCTGCCACCCAACCGAAGACGGTAACCCGTGTGACTTG
ACTGGAGAGAAGTGGAGATCTGATGTTCTCAGTGCCTTGTGATGATGAAGAACCGCAGA
TCCATCACTGGAGAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCACTGGCCACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGCCCTGAGTATATCAAGTACTTCATGATAAA
ACCATTGATGAGGAACAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCTTGCCTTATCTATGTCGACCTCCTTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATTTGACGCTACTGTGTTAGTACGGTAC
AAAGTGACACATACCCCTACCAAGCACTCCCTACCCGTATCTGTTCAAGGGCAA
GGAGGCAATGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAAACTTAAAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGTCA
TGGGAAAACAAGAAGATAAAAAGTCTCACTTGGCAGTGCTCTCTGTCAATT
CCAGGCTTTCCATAACCACAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCACTGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCTGCCATGCTGGCCAAGTGTTCAGTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCTCAAGCTGGTCAAGCTGTTAACGCTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCTTCTTCTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCAGGACTCTGCTTCTTAAGCCCTCTGGCTTATGGTC
TTCAATTAAAGTATAAGCCTAACTTGTGCGTAGTCCTAAGGAGAACCTTAAACCAAAAG
TTTTTATCATTGAGACAATATTGAACACCCCTATTGTTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTTGAGGAGAAATCCCCTGGACTTCAC
TAACCCCTGACACATCTCCACACCCAGTTGATGGCTTCCGTAAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCGAGGAAGCTGCCTGGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAAGATGGGCTTGTGCTCTGGTCCA
TTGCTCTGCTGCCGGCTCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAAGAACCTAGGCAACGGTCATGGCAAAGACCTCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT
GTGCGAGAACGGGGCCCAAGAGAAGGAGCTGCTGGTGGCCATCGGCTGAGGCACCGCTCT
TTGGGACTACCAAGGCCGCGTCACCTGCGGAGGACAAAGAGCATGACGTCCTCGCTGGAG
ATCCAGGATCTCGGCTGGAGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTCCCTTACAGTCCCCA
ACGGGCGCTACCACTTCAACTTCCACGAGGCCAGCAGGTCTGTGAGGAGCAGGCTGCCGTG
GTGGCCTCTTGTAGCAGCTCTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGGCC
CAGGCCCTGGCACCTGGCGTGCAGAGCTACGGCCCCGCCACCGCCGCTGACCCTATGAT
GTATTCTGCTTGCCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCTGGAGTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGGTTCACCCGATCTAACGTGGGCCCCAGAGCCTGGGT
CCGAAGCTTGGCTCCCCGACCCGAGAGCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATCTCCCTACTGGCTGTGTATTTATTGAGTGGTT
CGTTTCCCTTGTGGGTTGGAGCCATTTAACTGTTTTATACCTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCCAAATGCCCTCTTGCTCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCCATTGCGGTTTGTGGCTCTG
GAGGGTTCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGCCAGAGTGGC
GGTGGCCTGTCAGAATGCCGCCGGAGTCGGGAGCTGGGGCACAGTTCTCCCTGCC
CAGCCTGGGGAGAACAGGCCCTCGGGGCCCTCCGGAGCTGGGCTTGGGCCCTCTGCC
CACCTACTTCTCTGTGAAGGCCGTGACCCAGTCGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTAGGCTTCCAGGCAGAACATGAGGGAGGAAGAACCTCCCTCCCCGTCC
TCCCTCTGGTCCAAAAGAACATGTTTGTGTCATTGTTCTCTGTGTTCCCTGTG
GGAGGGGCCCTCAGGTGTGTGACTTTGGACAATAATGGTGTATGACTGCCCTCCGCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ
VCAEQAAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRLLHRYDVFCFATALKGRVVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQGDGSMATRE
ELTAFLHPEEFFHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAETLGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCTTCCGCACTCGGCGCAGGGGGTGGAATCTCGAGCAGGTGCGGAGCCCCGG
GGGGCGGGCGGGGTGCGAGGGATCCCTGAGCCTCTGCCCCCTTTGCGCTCCAG
CCTGTCGCTCGTGTGTTTGGGCCCGCCCTCCCAGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
GGCTTCGCTGCAATTGCGCCGAGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCTGCTGTCCTCTCTCTCGCCGGCGCCGGGATCGAAGGGGTGCGGGGCTCT
GAGGAGGTGACCGCGGGGCTCCCGCACCTGGCCTTGGCGCATTCCTCTCTCTCCCAG
GTGTGAGCAGCTATCAGTCACC**ATGT**CCGCAGCCTGGATCCGGCTCTCGGCTCGGTGTG
TGTCTGCTGCTGCTGCGCCGGGGCCCGGGAGCGAGGGAGGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTTGGACATCAGGAAAGAGAACAGCATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTGTATGGGAACATAGTATGATCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTAGCTACC
TGGTCGAGAAAACATTCTCAGTATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTACAGTAATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAACACCCAGAGAAGAAAATGG
CAATAAAAGATTGTAAGCAGCATTCAGTGTGATGGAGCTTAAATTGGGCAGC
GCCGATTAAATTACAGAAGATTGGGAGCTTGGGAAAGTGGCTCTAATGTTGGGAACA
GAAGGACACATGTCAGGACATCTTCAAGGCCATGAAACATCCAAAATAGAATTTCAGTGA
AAACTTTACATCAGCCAAAGATGTTTGTGCTTGCATAAAGGAAGTAGGTTAGGGGTA
ATTCACATACAGGAAAGCCTGAGCATACTGCTCAGGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGTGTTATTGATGGTGGCCCTCTGATGACAT
CGAGGAAGCAGGCATTGTCAGGAGAGAGTTGGTGTCAATGTTAGTCTGTGGCCA
AGCTTATCCCCTGAAAGACTGGGATGGTCAGGATGTCACATTGTCAGGCTGCTGT
CGGAATAATGGCTTCTCTTCTTCTTACACATGCCCAACTGGGACCCACAAAATACGTTAA
GCCTCTGGTACAGAACAGCTGCACTCATGAAACAAATGATGGTGTGAGAACCTGTTATACT
CAGTGAACATTGCTTTCTAATTGATGGCTCAGCAGTGTGGAGATAGCAATTCCGCTC
ATGCTGAAATTGTTCTTCAACATGCCAAAGCTTGAACATCTGGACATTGGTGCCAGAT
AGCTGCTGTAAGTTACTTATGATCAGCGCAAGGAGTTCACTGTTACTGACTATAGCAGCA
AAAGAGAATGTCTTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGAACAGCTACTG
GATGCCATTCTCTTCACTGTTAGAAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTCTAGTAATTGTCACAGATGGGCACTTGTGATGTCAGTGTGCAAGGGCTGCA
CACATGATGCAGGAATCACTATCTCTCTGTTGGTGTGGCCACTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCAAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTTCTTAAGATCCAGAACAT
AATGGTAACATTGACAACAGGAAAGAACAGTACAAGGGATCCAGTGTAATTGTTATT
CTCATATAACTGAAATGCTTACGCTACTAGAATCAGATAACAAACTATTAAAGTATGTCAC
AGCCATTAGGCAAATAAGCACTCCCTTAAAGGCCCTGCCTTCTGGTTAACATTACAGTGT
ACTTTGTTAAAACACTGTCAGGCTTCATAATCATGGCTCTTAGAAAACCTCAGGAAAGAGGA
GATAATGTGGATTAACCTTAAGAGTCTAACCATGCCACTAAATGTCAGATATGCAAA
TTCCATAGCTCAATAAGAACATCTGATACCTAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLPGPAGSEGA APIA ITCFTRGLDIRKEKADVLCPGGC PLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPV RVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQBEATGQAVSTAHPPTGKRLKKTP EKKTGNKDC KADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGT EGP HVGLVQASEHPKIEFYLK NFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDA GVRKGIPKV VVV FIDGWP SDDIEAGIVAREFGVN VFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTKYVKPLVQKLCTHEQMMC SKT CYNSVNIAFLI
DGSSS VGD SNF RLML EFV SNI A KTFE IS D IGA KIA AV QFT YD QRTE FST FDY STK ENV LAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDQGSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKD MASKPKESHAFFTREFTGLEPIVSDVIRGICRDPFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGGCCTCCCGACCCGGGCCCCACCGCGCGCTCCCGCATCTGCACCCGAGCCC
GGCGGCCCTCCGGGGAGCGAGCAGATCCAGTCGGGCGCAGCGCAACTCGTGTCCAGTC
GGCGGCCGCTCGGGCGCAGACGGAGATCAGCGGCTGGGGCACCCCTGCTGTGCCCTGC
TGCTGGCGGCGCTCCCAACGGCCCCCGCGCCGCTCCGACGGCAGCTCGCTCAGTC
AAGCCGGCCCGCTCTCAGCTACCCCGAGGAGGGACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACATTACCTCCCAGCTAT
CACAAATGAGACCAACACAGAACAGAAGGTTGGAAATAATACCATTCATGTGCACCGAGAAAT
TCACAAGATAACCAACAAACAGAACAGAAGGTTGGAAATTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGGAGCAGGGACATCATCAGCAGGACTGTGGCCAGC
ATGTAATGCCAGTTGCCAGCTTCACTGACACCTGCCAGGCCATGCCAGGGCAGAGGATGCT
CTGCACCCGGGAGCTGAGTCGCTGTGGAGACCGACTGTGTGTCTGGGGTCACTGCACCCAAA
TGGGACCCAGGGGAGCAGCATGGGACCATCTGTGACAAACAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCCTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCCTGGAGGGGA
GCTTGGCATGACCCCGCCAGCGGCTCTGGACCATCTCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGCACCCATGCCCTTGCCAGTGCTTGGCCTCTGCCAGGCCCCACAGCGCTG
GTCTATGTGTCAGCGCACCTCTGGGGAGCCCTGACCAAGTGGGAGATCTGTGCTGCC
CAGAGAGGTCCCGGATGAGTATGAAAGTGGCAGCTTCATGGAGGAGGTGCGCAGGAGCTGG
AGGACCTGGAGAGGGAGCTGACTGAGAGATGGGCTGGGGAGGCTGGCTGCCAGCCT
GCACCTGCTGGGGAGGGAGAGATTAGATCTGGACAGGCTGTGGTAGATGCAATAGAA
ATAGCTAATTTATTCCTCCAGGTGTGCTTCTGGGCTGGGCTGACCAGGCTTCTCTACA
TCTCTTCCCACTAAGTTCCCTCTGGCTTGACAGCATGGGTGTTGTGATTTGTTCA
TCCCCCAGGCTTCTCCAGGCTTCACAGCTGGCTTGGGAGAGTCAGGCCAGGGTTAAAC
TGGCAGGAGGAGTITGCCCCCTGTCAGGATATTGGCTGCTTGCCTACAGTTGGCAG
ACAGCCGGTTCTCTACATGGTTGATAATTGTTGAGGGAGGAGATGGAAACATGTGG
AGTCTCCCTCTGATTGGTTTGGGAAATGGAGAGGAGTCGCTTGCCTTGCAAAACATCAA
CTGGCAAATGCAACAAATGAAATTTCACAGGCTTCTCATGGGCTAGGTAGCTG
TGCCTTCAGTGGCAGATGAAATGTTGTTCTGGCTTCCAGGCTTCTCATGGGCTAGGTAGCTG
AGCAGTGGTCTCAGGCTCTACCTCTGTGCCAGGGCAGATTTCATATCCAAGATCAATT
CCTCTCTCAGCACGCCGGGAGGGCTATTGTTCTCTGTCCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGGCCAGTCACACAGCTAGTGAAGACAGAGCAGTTCT
CTGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCTTGGTGCACCAA
AAGTGTCTCCCAAAAGGAAGGGAGAATGGGATTTCCTGAGGCATGCACATCTGGAAATTAG
GTCAAAACTAATCTCACATCCCTCTAAAGTAACACTGTGTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGCTCTCTAAATGAAAGACAATGATATTGACACTGTCCCTCTTGCAGT
TGCTTACTGAGGTTAAATTGTAAGGGCAGGATTAAATGAAATTGCAAAATCTAGCAGAAC
TGAAGACAATTATCAACACAGTGGAGAAAATCAACACAGCAGGGCTGTGAAACATGGTT
GTAATATGGGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCTACCCAGAGTTCTTAAAGTTAAAGTGTGACATGATGTGTA
TAAGCATGCTTCTTGAFTTAAATGATGATAAAACATAAGTTGCAATTAGAATCAAGC
ATAAAATCACTCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEEMAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEII

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWAGATATVPVVPWHPCPPQACQCQIRPWYTPRSSYREATTVDCNDFLFTA
VPPALPAGTQTLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHAPQILSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLSESFYDNQ
LARVPRRALLEQVPGLKFLDLNKPLQRVGPGDFANMLLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMESTMLNNNNALSAHQQTVESLPPNLQEVLGHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCACEPPDLQRLPVREVFPREMTHDCHLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPTAGLRLTPAHAAGRYYRVYPCTLELRRRTAEEAGLYT
CVAQNLVGADTTKTVSVVVGRALLQPGRDEGGGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTOLACVWARTKEATS
CHRALGDRPGLIAILALAVLILLAAGLAAHGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSGETLPPQLSQQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGGCCAAGGCGCTGTTGAGAAGGTGAGAAGAATTCGGGACCATGTGGAGGAGGGGACATTGTGTAACGCC
CTCACATCGGCAGACCATCATAAGGTGATCAAGTTCATCCATCATCTGCTACACCGCTACTACGTGACAA
CATCAAGTTCGGAGCTGGACTCGACCGTGACATTGAGAGCCGTGACGGCTACCGCACCCTACCGCTGTGCCACCC
CTGGGCCAACACTCTCAAGATCTGGCTCTTCACTACAGCTGAGCTCATCTTACCGGCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCTCAAGAAGTACTGTGTTGAGTGTGAGCTGAGGAGAGCAGCTACAG
CGACATCCGGAGCTCAAGAACGACTTCCGCTTCACTGCTGACCTCTGAGCTGACCGCTCTACCTCCAA
GCCCTTCTGGCGTCTCTCTGCGAGGTGAGTGAAGAACAGCTGCGGAGCTGAACCTCAACAAGCTGAGCTGGCGT
GGCAAGGCTCCGGAGCGGCTCAACAGAACCGCAGGACAGCTGGAGCTGACCTGCTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGGCTCTGAGCTGAGCTGATCCCGAGCTGACCCATCCCGCC
CAGCAITGCCAGCTCACGGGCCCTCAAGAGCTGAGCTTACACAGGGCAAGATGAGCTGAGGCGCTCGCGT
GGCCTTCTGCGAGAGCGGCTGACATCACTGGGAGGACATCAAGGGAGATCCCCTGTGAGATCTA
TAGCTGAAGAACACTGGAGGAGCTGCACTGGGCAACCTTGAGGGAGAACACCGCTACATGCTGATCGA
CGACATCCGGAGCTCAAACGCCAAGGTGCTGGGCTCAAGAGCAACTAACAGCTGAGGAGCTCAAGGCCAAGCTG
AGATGTTGGCGTGCACCTGAGAACGACTGCTGACATCAACATGGGCAACAGCTCATGCTCTCAAGGCCCTAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGACCTGGGAGCTGGAGCTGGAGCATCCCCACTCCATCTGACCT
CCAACACCTGCAAGGAGATTGACCTCAAGGCAACAACTCAAGGACATGGGAGGAGATCATGAGCTTCCGACACCT
GCCACCCCTCACCTGCTTAACTGCTGAGCTACACCATGCGGACATACCCATCCAGATGCCAACCTCAAA
CTGGAGGCGCTTACCTGAGAACCTGCAAGGAGATCCCACCCAGCTCTCTACTGCCAACGCTGG
CTACCTGGACACTGAGCACACCTGACCTCTCCCTGGGACATCGGCCCTCTGAGACACTCCAGGAAACCT
AGGCCATCACGGCAACCGGATCGAGAGCTCCCTCCGGAGGACTCTCAGCTGGGGAGCTGGGGCCCTGGCCT
GGGCAACAACTGAGCTGACTGCTGCTCCCTCCAGGGTGGCGAGCTGACCAACCTGAGCAGATCGAGCTGGGG
CAACCGCTGGAGCTGCTGCGCTGGAGCTGGCGAGCTGCCCCACTGCTCAAGCGCAGCGCTTGGTGGTGGAGGA
GGGAGCTGTTCAACACA CACTGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG
GGGGCGTCAAGCACAGCAGGAGCTGGCCAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG
AACTCCCGGAACCCAGACAGCCTCCGGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAG
GGAGCTGATCTGGGGCTTCTCCCTCTGAGACTCACGGGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAG
AGCAACTCTCAAGGCCAGTATTGGATAATCAGGGTCTCTCTGGAGGGCAGCTCTGCCCAAGGGCTGAG
CTGGCACAGAGGCTCTGGGACCTCTACTTGGTATTATTATTCTCCATCTCCACCTCCCTTCATCC
AGATAACTTATCATCCTCAAGAACAGTTCAGGGAGGGTGTGAGGAAAGGTGGGCTGCGCTTCTCC
TTGCTCTTATTTAGGAGATGCCGGGGCATTAAACACCCACCTGGACTCTCAGCAGAGTGTGCGGGGAGAACAG
CCATGGGAGCTGCCAGCAGTGGGGCTGGGAGGAGCTGGGAGGAGCTGGGAGGAGCAGCCCTCAGCTGGA
AAGGGCAGGGCTGGAGCTTCTCTCTGAGTTTGTGGAGCTTTAGTTTTTGTGTTTTTTAACTAAA
AAACATTTTTTAAAGAAAAGCTTTGAAATAGTGGTTGGTATTTAAAAGAAAAAAACTTAAAAAAA
AAAAGACACTAACGGCCAGTGGAGGAGCTCAGGGCAGGGTGGAGGTTCTCCCTGAGCAARGCAGCCAGCT
TGACTGTTTCTTCCCTGGGGCAGGGTGTGGGTCTCCCTGGGAGGTTCTGGGAGGTT
CTATTGTTCTGGGAGGGAGGTTTGTGTTTGTGTTTGTGTTTGTGTTCTGGGAGGTT
ATGTGCTTGGCAGGACTCAATTCTGTGCTGTGCGCAGAGGGAAATGTTCTGGAGCTGCCAACGGAGGAG
ACTCGGGTGGCTAATCCGGGATGACGGTGTCCATTGGCAGGCTGGTCTGGGAGGAGCTGGGAGGAG
CCGACAGCTGAGAACAGGAGCCACTGGCCAGACTTGTGTTCTCCCACTCTGGGGCATGGGTGTG
CCAGTGCCACCCGCTGGCTCGCTCCATCAGGGCTGGCCACCTGGCTCTCATGAGAGCAGACACTTA
GAGGTGTTGGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGGTGTGTTCTGGGAGGAGCTGGGAGGAG
CTGGAGTGCACACAGCCAGTGGCACCTGGTGGCTGGAGCCACCTGGCTTAACTGAGCTTGGGAGGAG
AGAAGGGTCCCGCCTTGGATCAATCACCTGGAGACACTAAGGCACTGGTGGTCTGGTCTTAAATGATTG
CCATCTGAGAACCCATGAAGGAAAATCCGGTACATGTGGGTGTAACATGTTGAGACTCGGTACAGTAG
CCTCTGACAACCATGAAGGAAAATCCGGTACATGTGGGTGTAACATGTTGAGACTCGGTACAGTAG
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIICTVYVHNIKFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTLDKLRQLRTKNAQDKLELHLMFMSGIPDVTVDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENRLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRRLKVLRLKSNSLSPQVVTDVGVHLQKLSI
NNEGTKLIVLVLNSLKKMANLTELLELIRCDLERIPHISIFSLHNLQEIDLKDNNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKEIEKIPTQLFYCRKLRYLDLSSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLAHLGNNVLQSLPSRVGELENTNLQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

✓ amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGCATTGACT
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGCTATAATTGCAACCAACTCTGCAAGAACCTTCAGAACTGCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCTTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTAAACACCGAAAACCACCTGGCTCCAGGCTGCCAGTCTCTTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGGCATTAGCGAGGGACCATCAAGTGCAACTTGCGGGGT
TGCCCTGGGTGATTCTGGATCTCCCTGTGATTGGTCTCTGGGACCTTACCTGT
ACAGCATGTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTTCTATAACATCTTAACAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCAGAATTCACACAGAGCCACCTAGTTGTCTTGTCAAGCGC
CACCGTGAGACACCTACAACAGAGATGCCCTAACAGCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCC
GGTGGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCACTGAGCTGAAGTGGAAAGGCC
ACAGTGCACCTAAATCTTGGAAACATCTGCTTTGTCAAGCTCTACAAAGAACCTTGTCTTC
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGAGAGGATAAAATCATGTC
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GТИКCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGWGKAEMIIEQNNTDGVNFYNIILTКSTPTSTMЕSSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMLRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCGCGGGAGAGGAGGCCATGGCGCGCCGGGGCGCTGCTGCTGGCGCTGCTGGCT
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTACAGGACCATGCGGCCGA
CGGGTCATCACCGTCGCATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCGTGGCA
GGGGAGCCTGCGCCGTGGGATTCCCACGTATGCGGAGTGGAGCCCTGCTCAGCCACCCTGGG
CACTCACGGCGGCCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGGCCCTCGCTACCTGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCCCCACACCTCCAGGAAGTTCAAGTCGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCTGTAAAGAACATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATGCCACACTTGGATCCAGAAG
CTGATGGCCCAAGGTGGCATGTCAGGCCAGACCCCTCTGGCCACTACTTTTCCCTCT
TCTCTGGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCCTGCAAGGGATTCTTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLKRPEAQEAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSRLW
DSHVCGVSSLSSHRWALAAHFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLsapVTYTAKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVEQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSVWVGCGRPNRPGVYTNISSHFEWIQKLMAQSGMSQPDPSPWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACAGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGGCCCTGCCTCTAGGGCT
CTTGCCCTCATCTCTGGAAATGCAGTTACAGCCGGAGCCGACCAGGGAGGACGC
TGCCCCCAGGCTGGGTGCTCTGGCGCTGGGACCTTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCTCAATA CGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGT GAGGCCATCCC
CACTGACCCCTCACACGGTCAAAAAATGGCTCTTGGCAGCCGGAGCCAGAACAGTGCATTCT
GTGATCACACAGGACTTCTGACTTGTGCTGGCTGAGCATCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCACTACTATGTGGGAGGACCTACGGAAACCCATGTGTAAGGTCCCAC
ATCCCTACCAGCTTCCACAGGGCTTGGCCCATGTGGACTTTGTGAGGACTGCAACCGT
TTTCCCCCAACATCATCTCTGGAGCAACCTCTGAGGCCAGGTGACAGGGACTGTAGGGCT
GCATCTGGGGTAACCCCCTGTGATCGTAAGCGATAACA ACTTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCTGTGGCCAGTCTCTGGAGCAGTATTCTCATGAC
TCAGACCTGGCTCAGTTCTGGCCCTCTGGGACACTTGTGACATCAGGCATCAGTAGC
CCGTGTGGTTGACAACAGGGCGGGGGGGGGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGTGCTGGTGCACATCTCACCTGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGGACCCCTCTGGCTAGGCTCATGCTCTAGTAATGAGTCAGGCCCTGCCACATGT
GCATACTGTGACCTATGGAGATGATGAGCACTCCCTCAGCAGGCCCTACATCCAGCGGTC
ACACTGAGCTCATGAAGGCTGCCGCTCGGGTCTCACCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGTGGTCTGTCCTGGAAAGACACCCAGTCTCGGCTTACCTTCTGCCCTCAG
CCCCATGTCACACAGTGGGAGGACATCCTCCAGGAACCTTCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCA GCAATGTGTTCCACGGCCTTCAACAGGAG
GAAGCTGTAACGAAGTCTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CA GTGGCCGTGCCCACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGT CAGCAACA
GAGTGGCCCATCCATGGGTGCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGATCTTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCGCCCCCTCTGGCTTCTCAACCCAG
GCTCTACAGCAGCATGGGGCAGGTCTCTTGATGTAACCCCTGGCTGCCATGAGTCCTGTC
TGATGAAGAGCTAGAGGGCCAGGGTTCTGCTCTGGCTCTGGATCTGTAAACAGGC
TGGGAACACCAACTTCCAGTTGCTGAAGACTCTACTCAACCCCTGACCTTTCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCCTGAAGCTGGCAGTTCTGCTCTTATCTGCCCTGTT
GAAGCCCTGCTGAACCCCTCAATTATTGACTGCTGCAGACAGCTTATCTCCAAACCCCTGAAA
TGCTGTGAGCTTGACTTGA CTCCAAACCTCAATCATGCTCATCATCACTCAGGTCTCCCTACT
CCTGCTTAGATCTCTAAAGATGCTGTAACTAGCATT TGTGAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCCAAGGGTTGTATACAGACTCTGCACTA
TTTCACTTGATATTCACTTCCCAATTCACTGCAAGGAGACCTCTACTGTGACCGTTACTCT
TTCCCTACCCCTGACATCCAGAAACAAATGGCCTCCAGTGCTACACTTCTCAATCTTGCTTATG
GCCCTTCCATCATAGTGTGCCACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGCTCTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCTCATTG
TCCATTGTTAGATT TTGCTCTCTCAGTTACTCATGTCCTCTGAAACAAATCACTGACA
TCTACAACCAATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
A TGAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSFTFALRQQNVERLS
ELVQAVSDPSSPYGKYLTLENVALVRSPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSHPYQLPQALAPHVDFVGGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPSSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPWDPTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCCGGGCCACACCTGTCAGCGCGCAGCGAGCGCGGCCGGC
GGGCTGCTCGGGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCCTTCTC
TTCTTCTGCTGTGCTGGCAAGTGAGCCCTAACAGTGCCCCCTGGAAACCCACTTG
GCCGTGCAACCGCCCTCGTGTCTTGCCCAGTCTACCCCTAACCTAGCCAAGCCAGACT
TTGGAGCGAAGCAAATTAGAAGTATCTCTCATGTGGACCCAGTGTCTATGCAAGGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGACAGAGACGCAAGTGGGCATCTACATCCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTCAKGCACTTTGGAAAGGACTTCTGCTCAACTACCCCTTCTCACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAACGATGCTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC
□ AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTTCCACTCAGCCATGCCAGAGCATGAA
□ ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAACGGGTTGGATCAAGGGCAATGCCA
□ ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
□ TTTATGAAGATTGGGTGAGCCCTCTGTAAGCAGCTGCCAGGGGCAGAACATTCACTTCTC
□ TGTTTATGACAATGACCGACCAGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
□ CCTATGACTTGCCTTACCGCAATGCGATGCCAGCCAGGGGCCAGCGGGCTGGGTCTAT
□ GTGAGGATGTGAAAGAGACAGCAGCAGAACAGTGGAGCAGAAAATTATTGGCATTTCAGG
□ GCACCAAGTGGGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
□ CTCCTAAATATGCCAGATTGCTATTGGATAAGGAAACTACCTGGATTGTAGGGAGGGG
□ **TGACACAGTGTCCCTCTGGCAGCAATTAAAGGTCTTCATGTTCTATTAGGAGGGCC**
AAATTGTTTTTGTCACTGGCGTGCACACGTGTTGTTGTTGTTGTAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAACTG
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGGCATGAGGAATATTGACAATTAAAGTTAATCTTCACGTTTG
CAAACTTGATTTTATTCATCTGAACCTGTTCAAAGATTATTAATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLLFFLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCPGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVKG
TQKLRVGFLPKFKDGGRGANDSTSAMP
EQMKFQWIRVKRTHVPKGWI
KGNANDIGMDYDYA
LLELKKPHKRKF
MKIGVSPPAKQLP
GGRIHFSGYDNDRPGNLVYRFCDVKDETYD
LLYQQCD
AQPGASGSGVYVRM
WKRQQQKWERKI
IGIFSGHQV
WDMNGSPQDFNV
AVRITPLKYAQIC
YWKGNYLD
CREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCGTCCCCCCCCACCGCCATGGTGGTT
CTGGAGC GCCCCCAGCCCTGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATCGGCCAGGATACTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACGGGTTGTGGCGCGAGGACAGCACTGACAGCAGTGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTGCTCACCAAGCCCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTGGTCCAGAAGGTGGTGTGCTGGGTGGC
CCCACCCCTGTGATTCTGGAGGAAGGTGCTGTGAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCAACCTGATGCCCTATCCACCT
CCCTCAAACACCCACTGCTGGATCTCAGGGCTGGGGAGCATCCAAGATGGAGTCCCTG
CCCACCCCTCAGACCCCTGAGAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT
CTGACTGGGGGAGCAGGACAGGACCCATCACTGAGGACATGCTGTGCGCGCTACTT
GGAGGGGGAGCGGGATGCTGCTGGCGACTCGGGGGGGCCCTCATGTGCCAGGGACG
GCCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCAGGGCTGTGCCGAGGCCAACAGGCC
GGGCTCATACATCAGCCTCTGCGCACCGCTCCCTGGTGGAGAACATCGCAAGGGTGCA
GCTCCGCGGGCCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCG
CCGCGCGCTCTAGGGCGCAGCGGGACCGCGGGCTGGATCTGAAAGGGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCCCTGGCGGTTCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTGCCAAAGGAAACCCCTCCCGACCCGCCGAC
GCCCTCAGGCCCCCTCAAGGCATCAGGCCCGCCAAAGGCCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGGCCCCGGCCCCAGCGCTTTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCTGCCACATATCTTATTCTCCAATTCAATAATTATTTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAAIRIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWRVITAHHCFKDNLNKPYLFSVLLGAWLGNPGRSQKVGVVA
WVEPHPVYSWKEGACADIALVRRLERSIQFSSERVLPICLDPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCShLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCACTGCTA
CTGCTGGTGGCCACCAAGCCCCGTTGGACCCCTCACAGATGAGGAAAAGCTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGTCACATGA
GATGGGACGAGGAGCTGGCCCTCGCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAGGAGCGGGCGCCGCGCGAGAACTCTGTCGCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAACACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCCACTACACGCAGGTGTTGGCCAAGACAGAGGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAAATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCAATGTCCTCTGGCTACCACGTCAAGAACTCCCTCTGTGAACCCATCGAAGC
CCGGAAGATGCTCAGGATTGCCCTAACCTGTAACGTAGGCCCATCCTCCGGGCCACTGA
AGCATCAGACTCTAGGAAAATGGTACTCCTCTCCCTAGCACCGGGATTCCGGCTTCT
TGGTAACAGAGGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTGGAAACCCAGGC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAAAC
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCACCCATGCCAGGAGGAGGTGAGGCTGAGGCTGAGTTGCCCTTCCAGTG
AGGCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAACCTCTGCCACGCCAA
TGCCACGGGTGGCGTGCCTGGCTGCACTGGCTTGCCAGGTGCAAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTTGGGCCCTCTCTGG
CTACTGCTCCTGCCCTCTGGTGTGGCTGGAATCTTCTTGATGGGATACCAACTAAAGGG
TGAAGAGGTCACTGTCCTCTGTCACTTCCCCACCCCTGTCCTCAGGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTCCTCATCACACCATCC
ATCCCTGGAGGGACAAGGCCCTGGCTGGCTGCCAGCTCAGGAGGCCCTGAGGACTGCCACACC
GGGCCACACCTCCTGCCCTCCCTGGCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCAACCTGGCTGGGCTGTGCCCACACAGCATGTCGCTCTCCCTGAGTGGCCTG
TGTAGCTGGGATGGGATTCTAGGGCAGATGAAGGACAAGGCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPPLLVLVATTGPGVAGLTDEEKRLMVELHNLYRAQVSPТАSDMLHMRWDEE
LAAFAKAYARQCVWHNKERGRGENLFAITDEGMVDPLAMEEWHHREHYNLSAATCSPGQ
MCHYHTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGRPYQRGTPCSQC
PSGYHCKNSLCPEPIGSPEDAQDLFYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPVCVTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGEQLQATLDHTGHSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNNSGPGVWGPILLGLLLLPPVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTCAGGCTTTCAATTGGGAAGCCCCCTAACAGAATCGGTCAATTCCAAGTTATGGTGGACGT
ACTCTGTGTCTCCCTCTGCTTGTTCATCATTAGCAGACCGGACTTAAGTCACAAACAGATTATTCAT
CAAGGCAGGTTCTCATGAGCCACCTCAAAGCCTCGAGAAGTGAAACTGAAACACAATGAATTGGAGACCATCC
AAATCTGGGAGCATCTGGAAATATTACACTTCTCCTTGGCTGGAAACAGGGATTGTGAAATACCTCTGA
ACATCTGAAAGAGTTCTAGTCCCTTGAACACTTGGACCTTAGCAGCACAAATATTCAGAGCTCCAACTCATT
TCAGCCTAACAGTCAAATATCTCTATCTCAACAGGAAACCGAGTCAACATCAATGGAACTTGGGTATTGACAA
TTTGGCAACACACTCTTGTGTTAAAGCTGACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACT
GCCCCAACGAACTGCAACATCTCGAATTGAAACCGAAACAGATTAAGATGAGTGGACTGACATTCCAAGGCTTGG
TGCTCTGAAGCTCTGGAAAATGCAAAGATGGTAACGGAAACTTATGGATGGAGCTTITGGGGCTGAGCAA
CATGAAATTTGAGCTGGACCATAACAACTAACAGGATCTGGCTTACGGCTTCTGATGCT
GCAGGAACCTTCATCTCGACAAAATGCCATACAGGATCAGGCCATGGCTGATCTGGAGATTCTGCCAGAACGTCAG
TGAGCTGGACCTAACATTCAACTCAGGTTAGTGTGATTCAAGGTTAGTGTCTCCCTGGCTAAGCTTACTAATAC
ACTGCACATTGGGAAACACAGAGTCAGTACATTGTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATAATGAAATTCTGGGATATTGAGACATGAATGTTCTGGCTTCAAGGAAACTGAG
GGAGCTGATACTCAAGGAAATCGGATCGCTTATATCTAAAAACGGCTCATGTTTGAGTCACTGGAG
TCTAGACCTGAGTGAACAGCAACTATGTTCTTACAGGCAATGAGCTTTCACAAATGAAAGAAAATCTGCAACAAATT
GCAATTAAATACATCAAGCTTTTGGCAGTGGCAGCTAAATGCTTCCCACAGTGGGTGCGGAAACAACTT
TCAGAGCTTGTAAATGCAAGGTTGTGCCATTCTCAGCTGCTAAAAGGAGAACGATTTTGTGTTAGCCAGA
TGGCTTGTGTGATGATTCTTCAACCCAGATCAGGTTACGGCAGAACACAGTGGCAATAAAAGGTC
CAATTGAGTTCTCATCTGCTCAGCTGCCAGCAGTGTATTCCCAATGACTTTGCTTGGAAAAAAAGACATGA
ACTACTGCATGATGCTGAAATGGAAAATTTGACACACTCCGGGGCAAGGTGGCAGGTTGATGGAGTACCC
CATCTTGGCTGGCAGGTTGGAAATTCTGGCAGTGGGGAAATATCAGTGTGATCTCCAACTTTGTGTT
ATCTTACTCTGTCAAGGCAAGCTTGGAGTACAGGTTACGTTACATGCTTACCAAGGCCCCATGGATCTCACC
CCAGCTGGGGCATGGCACGGCTTGGAGTGTGCTGCTGGGGCACAGCAGTGTGAGTGGCAGGAG
GGGGGACAGACTTCCACGCTGCACGGGAGAGCAGCAGTGTGAGTGGCAGGAG
GGATGTGAAGATAGAGGACATTGGGATATCAGCTGCACAGCTCAGGAAACTTACAGCAAT
AACTCTGACTGCTTCAAAACCATATTCTTGGCAGCTTGTGAGGCAACTGTAACAAAGGAGAAACAGC
CGTCTCATGCTGATCTGGAGGAGGAGCCCTCCCAAATGAACTGAGGACCTTGGGCTTGTGTT
ATACACATGTGAGATGCTAACACCTTGGCAGTGAAGGAGAACAGTGGCCCTAGTGTGATCCCCACTCAAC
CTGGGACTCCCATGAGTGAACAGGCCATTGGAGCTGAGCAGTGGGCAACTGTGGTGTGCTGATCATAG
CTGGGACTTGTCTGTGTTGGGGCGTGTGGTGTGCTCATATACACACAGGGAGGAATTAAGA
TTGCACTTACAGGATGAGGAGCTTGGGACCTGGCATATTGACAATAGCAGTGAAGCTGATGTTGG
AGCTGAGCAGGAGGATGGTGTGCTTCAAGAAAGTGGAGGCAACCCAGGTGTGCACTCATCTCAGGTCTGG
ATTTTCTTACACACATGACAGTGTGGGACCTGGCATATTGACAATAGCAGTGAAGCTGATGTTGG
CAGAGATCTGTTCTTGTGCTTGGGTTGGGACTTGTGCTCATCTCAGGTCTGG
TCTTGGAAACATATCATACAGGTTCTGAGCTTGTGCTTCAAGGAAAGCAGTTTAAATGGACACTATGAG
CATAAAGGAAAAGGAGTGTACCCATGTTCTCATCTTCAAGAAGATCTGGCAACGGAGCTTCAAGTAAATATAC
GTGGCCTTACATGTGAGGAGGAGCTTACAAACTAGTGTACTCTCAACATGAAAGACCTTGGAAATGAAAATCTG
TCTAAACAAGTCTCTTGTGAAATCCAGGAGCTGGCTCGTTGCTCGAGTAATTCTTCTG
TACCTTGGGAAAGCTCTCAGGAGACCTCACCTAGATGCTTCAAGCTTGGACAGCCATCAGATTGTGAG
AAGAGCTTATTTGAAAGCTCATCTTCCCGACACTGGACTCTGGTGTGAGGAGAATGGGAAAGAAAGGAC
AGATTTCAGGAGAAAATCACATTGTACCTTTAAACAGCTTGTGAAAGAAACTACAGGACTCCAAATTTTCTG
TTATGACTTGGACACATAGACTGAATGAGACCAAAAGGAAACGCTTAAACATACACTTCAAGTGAACCTT
AAAGAGAGGAATCTTATGTTTAAATGGAGTTGAAATTAAAGGATAAAATGCTTATTATATACAGAT
GAACCAAAATCAAAAGTTATGAAATTTTATCTGGGAAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACCTTGTGTTATGCAAAAGTATCTAGCTAAATTATGATATAATCATGATTATTTATGATTT
TTAAATGCGGAGATTCTTTATGAAAATGACTTAAAGCATTAAATAATACCTGGCTTGTACCATTTT
TTAAATAGAAGTTACCTCATTATATTGACACATTATTTAAATAATGTCATTTGAA

FIGURE 102

MVDVLLLFSCLLFFHISRPDLSHNRSLFIKASSMSHLQSLREVKLNNELETPNLPVGSAN
ITLLSLAGNRIVEILPHEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLTLNSNRVTSMEP
GYFDNLANTLLVLKLNRNRISATPPKMFKLPLQHLELRNPKIKNVGDLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMELILQDHNNLTETKGWLGYLLMLQBLHLSQNAINRISPAWE
FCQKLSELDLTFNHLRLDDSSFLGLSLLNTLHIGNRVRQYIADCAFGRGLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLLQGNRIRSITKKAKFTGLDALEHLLSDNAIMSLQGNNAFSQ
MKKLQQLHLNTSSLCDCQLKWLQPQVAENNPFQSFVNACAHQPLLKGRSIFAVSPDGVCDF
DFPKPQITVQPETQSAIKGSNLSCFICSAASSSDSPMTFAWKKDNEELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVisNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHAPQIAWKQDGTDFFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTGETAVLQCIAGGSPPPQLNWTKDDSPVVTER
HFIAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGVNRLSVIPTPTCDSPQMTAPSLLDDG
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLLAD
RQDGYVSSESMSGHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPPDRTVLMDHYEPSYIKKKECYCPSHPESEESCERSFSNISW
PSHVVRLLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFCOPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGTGGTCCTTGCAAAATG
AAGGATGCAGGACCCAGCTTCTCTGGAACCGAACCGAATGGATAACTGTGTCAGAGAGAACGGAAAC
GAACGCTTTCTCTGTGAGCCCTGGATCTTAAACAAATGTGTATGTGACACAGGGAGCATTCAAGATGAAA
TAAACAGAGTTGAGCCGGGGGGTTGGTGTCTGACATAATAATCTTAAGCAGCTGTCCTCC
CCACCCCCAAAAAAAGGATGATGGAAATGAAGAACCGAGGATTCAAGAAAGAAAAGTATGTCTTCTC
TATAAAGGAGAAAGTGTGAGCCAAAGGAGATTTTGGAAATGAAAAGTTGGGGCTTTTGTAGAAACTAAAGAAC
GGTGTGGTGTGTTCTTCTTTGAATTCCCAGAGGGAGAAATTAATAGATCTGCAAGAAA
TTTCAGAGAAAGAAAGTGTGAGCCGGCGAGATTGAGGCAATTGAGTTGGGGAGAGAACCCAGCAGCACAGTGG
TTTGCTCTATGTGACTAAAATTGAGGATACTTGTGAGTTGGGATTTCTCATCAACCTCC
TTTATTCCCTTGTGATCAAGATCATCGTTCTCTGTGAGGATTCCATGGATGTTGCT
GTGATCAGTGTGAAATACAATGTTGAGTCCAGGAGAACACAGATAAAATTGAAATGTTGAACAGAAT
GACCTTACATCCACAGAGATAATGAGTTCAAGGCTTAAACGGCCCTTATTTGACCCCTGCTGTGGTGT
GCTGGCTCTTCAACTCTGTGGTGGCTGGTCTGGTGGCTGGCTCAGACCTGCCCTCTGTGTCCTGCA
CCAGTTCAAGGGTGTGTTGTGCGGGCTGGTCTGGTGGCTGGGAGGATCTCAGGAGGCT
GCTGAAACCTCCATGAGAACCAAATCCAGATCATAAAGTGAACAGCTTCAAGCAGCT
ACAGTTGAGTAGGAAACCTATCAGAACATTGAAATTTGGGGCTTCAAGGTTCTGGCAGAACCTCAACACTGTG
ACTCTTGTGACAATGCTTACATCCACCTGGGAGATGGAGCTTGTGAGTTGAGCTTGTG
GGCAAACACCCCATGGAGACCTTCTTATGAGGAGCTTCTGGCCGACTAGACTTGTG
GGATTTGAAAGAACCTTGTACATCTGAGAGTGTGTTGGAGGTTCTGGCAGGTT
CATGTGCAACCTCGGAAATCCCTAACCTCACCGCTCATAAAATGAGTGAGCTGGATCTTCTGGGAGATCA
CTTATCTGGCATCAGGCCGCTGGCTCTTCCAGGGTTGATGACCTTCAAAATGTTGGA
TCAGTGTGAGTGAACGGAAATCTTGTGACACCTTCACTGGTCAACT
ATTACTGCTCATGACTCTGACTCTCCCTGGCATCTAGAGCGGATACATTAC
TAACCTGTGACAATCTGGTCTGAGCTGGTGGATAAAAGACATGGCCCTCGA
TAACACTCCCTCCAACTTAAAGGGAGGTTACATTGGAGAGCTGAGGAAATTACT
GATTTGGAGCCCCCTGCAAGGCTCAATGACTGAGGCTGGAGCTGAGCTG
CTTGACATCTGATCTGGATTACTCCAAATGGAGACTCATGACACATGGGGCT
GCTCAGTGTGGTACGTTAAATTCACAAATGTAACATGCAAGGATACAGG
TTCCGGTGGGAAATACTACTGCTTCAAGGACCCCTGAATGTTACT
AACCGTCACAGTAGAGACTATGGAAACCCCTCTCAGGATGAGGACGG
AGTTGGTCGACTGGAGACCAACTGGTACCCAGGAATTGATGGAGG
CACCACCTCCAGTGAATATAAACAGTGGGATCCAGGAATT
TGGGTGTTTGIGGCCATCACACTCATGGCTGAGTGTGGTCATT
TGGGAAACAACTCACCCCCCCAACAGGACTGTTGAATATTAA
CATGGAAAGCCACCTGCCCATGCTGCTATCGAGGATGAGGACCC
CAACCCACACAAACAGTTAACACAAATTCTACATACAGT
CTCTAACAGACATGTACAAGAGACTCAAATCTAAACATT
GACAGTTTATTAACAAATGACACAAATGACTGGCTAAATCTACT
AAAACATTACAGAGTTACAAAAAAACAAACATCAA
AAAAGAAAAGAAAATTATTATTAAATCTTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRATCPSCSNSQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIICKVNSFKHLRHLIEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLLRDLGELKRLS
YISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQLSVEINLAHNNTLLPHDLFTPLHHLERIHLHHNPWNNCNDIL
WLSWWIKDMAPSNTACCACRNTPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSWSWITPNGTVMTHGAYKVRIAVLSDGTILNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAAATTTPFSYFSTVTVETMEPSQDEARTDDNNVGPTPVWDETTNVTTSLTPQ
STRSTEKTFTIPTVDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPILLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLCAVLGRAGRSDSGGRRGELGPQSGVAAERPCPTTCRCLGDLDCSR
KRLARLPPEPLPSWVARLDLSHNFIKASSMSHLQSRLREVKLNNNELETI PNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNI SELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRNRI SAIPPKMFKLQLQHLELRNPKKVNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNSMEILQLDHNNLTETIKGWLYCGLMLQELHLSQNAINRISPDAWEFC
QKLELDLTFNHLSRLDDSSFLGLSLNLTIHGNNRVSYIADCAFGRGLSSLKTLDLKNNEIS
WTTEEDMNGAFSGLDKLRLRLLIQGNRIRSIKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHNTSLLCDQLKWLPOWVAENNQSFVNACAHQQLLKGRSIFAVSPDGFWCDDF
PKPKQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKDNLHDAEMENYAHLRAQGGE
VMEVTTILRLREVEFASEGKYQCVISNHFGSSYSVKALITVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHGPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCQAQNSA
GSISANATLTVLETPKFLRPLLRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGERGVRLSPVTPTCDSQMTAPSLLDDGWA
TVVGVIIAVVCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQ
DGYVSSESGSHHQFVTSGAGFFLPQHDSSGTCHIDNSSEADVEAATDIFLCPCFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHDHYEPSYIKKKECYPCHPSEESCRSFSNISWP
HVRKLLNTSYHNEGPGMNLCLNKSSLDFSANPEPASVASSNSFMGTGKALRRPHLDAYS
SFGQPSDCQPRAFYLAHKHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSLRHRLETILNQNRRLTSGLPEKAFFEHTNLNYLYANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPVLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDGLDN
ETFWKLSSLEYLDLSSNNLRSVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERPVPSGLPVRVTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLIDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGAGGGGGCTCCGGCGCCGAGCAGACCTGCTCCGGCGCCCTCGCCGCTGCTCTCCGGAGCGGCCAG
CAGTAGCCCCGGGGGGGGCTGGGGTTCCTCGAGACTCTCAGAGGGGGCCCTCCATCGCGCCACCAACCC
CAACCTGTCTCTCGCCGCACTGCCTGCGCCCAAGGACCCGTCGCCAACATGGATTTCTCTGGCGCTGGT
CTGGTATCTCGCTACTCCAGGGGGCCCGAGCTGCCCAGGAAATAGTGTCATCGAT
TGGCTATGTCTATGGGGAGGATTGACTGCTCTGGGCTGGCTGCCAGTCTGGGAGCTGTCAGCC
TGTGGCCAACCCAGTCAAAACATGGTAATGTTGGCCGAGCTGAAAGCAGGTGATCCCTGGTTATGCTGG
AAAACCTGTAACTCAAGATCTAAATGAGTGTGGCTGAAGCAGGGCTGTAAGCACAGGTGATGACACCTTA
CGGCAGCTAACAGTCTACTGTCTCACCGGATAATGCTCATGCCGATGTTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAGAACCTCTCGATGGCTGATGGTGTAAAGGCAAAATACGGTGCCAGTGCCTCATCCCTGGCCCT
GCACCTGGCTCTGATGGGAGGACTGTTGAGATGTGATGTCAGGAAAGGCCCTCTGCCCTAGATT
TAGGCAACTGTGTCATGACATAGACAGGAACTGTCAGTATGGCTGAGCAGCTTGTGATGTTATA
CAAATATCAATGTCATGACATAGACAGGAACTGTCAGTATGGCTGAGCAGCTTGTGATGTTATA
CGTAGCTGGGCTTACAAGTGCATAAAGGATACCAAGGGTGTGACTGACTGTGTATATCCAAA
AGTTGATGTTGAACTTCAAGGTCATCTGGAAAGTACTGGTGGCTCAGAACCCATATATCCCTCAT
TAATAATTGGATTCTGTGATGTTGGAAAGTACTGGTGGCTCAGAACCCATATATCCCTCAT
CAGGCCTACTTCAAGGCAACAAACAGGACTCACAAAAGGCAACACCAATTCTTACTCCACCAACCCACCC
CTGGCCACAGAGCTGAGAACCTCTGGACCTACCCACTGAGGAAAGGCCAACCCAGGACTGACAACTATAGC
ACACAGCTGGCAGTACCCAGGAGGATTACAGTGCACAGGAGTACAGACAGACCCCTCAGAAAACCCAGG
AGATGTTGTTGAGTGTGTTGGTACAGTGTGATTTGACATGGCTGAGTGTGATGAGGAGAAAGACAA
TGACTTGCACGGGAAACCAATCAGGGACCACAGGGTGGACAAATATCTGACAGTGTGCGCAGC
GGGAAAGCTGACGGCTGACTCTGGCTCAGTCACTGGGCTCAGTCACTGGGACCTGTGCTGTGAT
CAAGGTGACGGGGCTGACTCTGGCAACTCAGGGTGTGAGAAAACACGGTGCACAGGAGCAGCCTG
GGAGAAGAAATGGTGGCCATGGCTGGAGGAAACAGATCACCTGGCAGGGCTGACATCAAGAGGCAATCACA
AAAGATGATTAAAGGGTTGGAAAAAAAGATCTATGAGGAAAATTAAGGAACGTGGGATTATTGAGCTGGAGAAG
AGAAGACTGAGGGGCAACCCATTGATGGTTTCAAGTATATGAGGTTGGCAGAGAGGGTGCGACAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTAGACTAGAGTATAAGGAGCATTTCTGGCAG
GGCCATTGTTAGAATCTTCAAAAAAAAGAGTGTGAAAATCTCAGATCTCTCTCTCTCTCTCT
TAAAAAATTGTCATTTAAAGATGGTAAAGATGTTCAACCCAAAGGAAAGTAACAAATTATAGAATTTC
AGATGTTTGTACTCTACTAGTAGTGTGAGTAAACCTTTAGAACTAAATAATTGGACAAGGCTTAATT
CATTTCCCTCTTGACCTCCCTAAATGGAGGGATTGAAAGGGGAGAGGCCACCAATGCTGAGCTACTG
TCTCTCCCTATGGCAATCTGAGTATTAAAGAAAAGGAAACATTATCCAAATGAGAGTATGAGGAC
AGATAATTGAGTATCTCAGTAATGCTCTAGTGTGCGGTGTTCAATGTTCTCATGTAAGGTTAAGGC
TTCTCATTTGTCATGGATGATGTTAGATTTTTTTAAAGAGATCTTCAGGAAACACAGTTCAGAGAG
ATTTCATCGGGTGACTCTCTGCTGTGAGTATCTGGCTGCTGAGAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTCCCTCACTCATGAGTGTGAGTTCAGTTCTCTGCTCATTTAACTGGTAAAGGAGGGCTGG
AGAACAGTAATAATTTTGGACAATAGGCTACAATAGAGGCTTCTGAGTATGAGTCAATTAAAT
AGGGGGAAAATAATCATTAGGCTTGGAGTAAAGGGAAAATAATGAAAGAAATTTTACTTTGAGTGC
TCTCTTATGGTCATATAACTGCAAGCTGAGATGAAAGGAGGAAATAATGAAAGAAATTTTACTTTGAGTGC
TGATACATGCACTAAACATGAGGAGAAGTTCAAAAGTACTGTTAACATCTGTTTATTATTTAAAT
CTAAAAAATTTGGTGTGTTCCAAATGGCTAATAAAAACAATTATTGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGGQIRCCPSPGLHLAPDGRTCDVDECATGRASCRFRQC
VNFTFGSYICKCHKGFDLMIIGGKYQCHDIDECSLGQYQCSSFARCYNVRSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSQLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPAQQYLTVSAAKAPGG
KAARLVLPLGLRMHSGDLCLSFRHKVTGLHSGTLQVFVRKGAHGAALWGRNGGHGWRTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGTGATTTGCCCTTAGTTGATGG
AATGGGCTCAAGGCTTACAACACTTCCCTTGCAACAGGTGCTTGCTCGGGCTGA
AGGTGACAGTGCACATCACACACTGTCATGGCGTCAAGGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCCA
CAAAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGTTCTGACTTGGAATACCC
AACACAAGTTCACCATGATGCCAACATGTCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAAGGCAATTACATCGTAAGGTCAACATTGAGGAATGGAACACTTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTCAAAGCAGTGGTGCAGATTCACTCCCT
CTGGGGCTGTGGACTATGTGGGAACATGACCTGACATGCCATGTGGAGGGGGCACTGG
CTAGCTTACCATGGCTAAAAAATGGGACACTGTGTCACACAGCTCCACCTACTCTTTTC
TCCCCAAACATACCTTCATATTGCTCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCTGGTGAAGGAAACCTGTCAGTGAATGGAAAGTGTGATATTGCCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGTGAAAGGCTAAAGTAGGGGAAGTGTGTTACTGT
TGACCTTGGAGAGGCCATCTTGTGATTCTGCTGATTCTCATCCCCCAACACCTACT
CTGGGATTAGGAGGACTGACAATACTACATATATTCAAGCATGGGCTCGCTTAGAAGT
GCATCTGAGAAAGTAGGCCAAGAACATGGACTATGTGCTGTGCTTACAACACATAAC
CGGGCAGGAAGGAAACTCATTCACAGTTTCAACTGTTAGCAAGTATAACTGGAATATCACTATTGATT
ATATCCATGTCTCTCTCTGTGAAAGGAAACCTACAAAGGCTTAAAGGAGAT
GCTAAAGGAGGCCAGAAACAGAAATCAGGAAAGCTCAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTGGAAATATGAAATTGTTGCTTTCCAGATGTTCTGGTGTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCTCTGATGTGATCGGGCAAGATTGACAGTACAGT
GTATGAAAGTTTCAAGCACATCCCTGCCAGCAGCAAGGACATCCAGAGTGAACCTTCTG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTTTAAAGGAAAACAGTGAAAAGT
ATATTAACTGGAATCAGTGAAGAAACCAGGACCAACACCTTACTCATATTCTTACA
TGCAGAAATAGAGGCATTATGCAAAATTGAAACTGCAAGGTTTCAGCATAACAAATGCTT
GTGCAACAGAAAACATGTTGGGAAATATTCTCATGTTGAGAGTCGTTCTCATGTCAGCG
GGAGAACGAAAGTGCACAGGGTTCTCATAAAGTTGTGAAATATCTCATACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGCTCACCTACAAA
TGTGGAAACATTACATTGTTGATTTTCAAGCAGACTTTGTTTATTAAATTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTGTTATTGACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCCTCTCTTTTTCAATCACC
AGTACTATTGAGAAGAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTCAAGGAAAGATGGATTCAAAATAATTCTGTTTGTCTTTTAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMNLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEIDIGNYSCLVRNPVSEMEDSIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNNTYIICKHGPRLLEVASEKVAQKTMDDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPTEYRKAQTFSGHEDALDDFGIYEFAFPDVSGVSRIPRSRVPAASDCVSGQDLHSTV
YEVIQHIPAQQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGGCCCTCGGGACTTGCAGTCCCCGGCAGTCCTGGTGTGTT
GCTTTGGGTGCTCCCTGGACGCACGGGCGCGAACGCAACGGTGCCTCATCACGGACAGA
ACTGGAGAGAACCTGCTGGAAGGGAGACTGGATGATAAGATTATGCCCGTGGTGCCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCAGGACTCGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGAGTGGTAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATACTGATAAAAGACTGGAAAGAGTATTGAGCCCCTTCATCATG
GTTTGGTCCAGGTTCTGTCATGAGTAGTATGTCAGCACTCTTCAGCTATCATGTTGA
TCAGGACGTGCTACAACCTTATTGAAGACCTTGGATGCGAGTGTGGGGATCATATACT
GTTTTGCTTGAACACTGTTTCCGGATGTTATTAGGACTCTGTATGATAATTGTC
AGATTGCCCTTGCTTCAAAAAGCGCAGACACGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAATCTGCACAAACCTTTGAAAAGTGGAGGGAGAACAGGGCGATGAAGAA
GATGTTCTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC
CATAAAGACAACGCTCTGGGTCATTTGCAACAGATAATCCTAGTTAAATTTTAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGGTTGGTTGAAGTG
ACTGTCGACTTTTGATATTGCGAGGTTCTAGCTAGATTGTCATTAATTAAGAGACTCTA
CATTGAGACATAAAAGCACTAGGTATAAGTTGAAATATGTTAAGCACAGTATGATG
GTTTAAATAGTCTCTAATTTTGAAAATCGTGCCTAACAGAATAAGATTATGTTATTTGT
TTAATAAATAACCTTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGATTAT
TGAGGTATTGAGAAGATTATTGAGAAAATATTCTCATTTGATATAATTTCCTCTG
TTTCACTGTTGAAAAAAAGAGATATTCCCATAAATGGGAAGTTGCCATTGTC
AAATGTGATTCTAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCCCTGT
ATTTTAGGTTATGCAACTAAAAAACCTTACCTTACATTAATTACAGTCTTCTACACA
TGTTAATACAGGATATGCTACTGATTAGGAAGGTTTAAGTTCATGGTATTCTCTGGATT
CAACAAAGTTGATTCTCTGTATTTCCTACTTACTATGGGTTACATTTTTATT
CAAAATTGGATGATAATTCTGGAAACATTTTTATGTTTACTAAACAGTATTGTTGTT
GTTTCAAACTGAAGTTTACTGAGAGATCCATCAAATGACAATCTGTTGTAATTAAATT
TTGCCCACTTTTCAGATTTCATCTTGTGAACTTCACCTGAAATTGTTTTT
TTTCTTTGGATGTTGAGGTGAACATTCTGATTTTGCTGTGAAAGCCTGGTA
TTTACATTGGAAAATTCAAAGAAGCTTAATATAAAGTTGCTCTCATACAGAAAGTCTTAATGAT
TTACAGTCTGTAATGCTTGATGTTTAAATAAAACATTTTATATTGTTAAAAGACAA
ACTTCATATTCTCTGTTCTTCTGACTGGTAATATTGTTGGGATTTCACAGTTAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTCCTACTCTTAAAGAGCTAGAAATACATAGTTT
CACCTTAAAGAAGGGGAAACATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCTCTTCTAGGCTCTGTTGCTGTGAAATCATTAGATTACAG
TATCTGTAATATAACAGTTCTTAAAGGCCCTCTCTTGAATTTAAATATTGTA
AAAGAGTTGGATGTTGAACTGTGATGCCCTAGAAAATATCCTAACGACAAAATAACCT
TTCTAACCACTTCATTAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACATAATTCAACAAACGGGACCCCTT
CTGTGTGCCAACCGCAAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGCTGC
ATTGCTGATGGCCTGGTTGGTCTGAGCTGTGTCAGGCGGAATTCTCACCTTATTG
GGCACATGACTGACCTGATTATGAGAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATAAGAGCTGGGCCAACAAAATGGAAGGCTTGAC
TAGCAAGTCACTGCTGATGCTGAGGCTACCTGGTCAACCTGTGAATGCTTACAATCTGG
TGAAGCGGCTAACACAGACTGGCTGCGTGGAGGACCTTGTCTGCAGGACTCAGCTGA
GGTTTATGCCAACCTCTGTGAGGGCAGTTCTCCCAACTGTGATGAGGACGAGATAGG
AGCTGCCAACCGCTGATGAGACTTCAGGACACATAACGGCTGGGACCCAGGACAAATTCTCA
GAGGGGAACCTCAGGACCAAGTACCGGCAATGCTGAGTGTGATGACTGCTTGGATG
GGCGCCTGCCAACATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCAGGGGGAGGCCAACCAAGTACACGGTGTGGACTACCTCA
GCTATGCTCTTCCAGTGGGTATCTGCACCGTGGCTGGAGCTCACCGCCGCTGCTC
TCCCTTGACCCAAAGCCACGAGCTGGAGGAATCTGGGTACTTTGAGCAGTTATTGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGGGCTGTGACTACTCTGCTGAGAGGGATGTTTACAGAGGCCCTGTCGTGG
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAAGAGGCTTCTGTTAGGATACCACATGGCA
CAGGGCCCCAACAGCTGCTCATGGCTTCAAAGAGGGAGGAGCTGGGACAGCCCCACA
TCGGTCAAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA
CTAAACTTGACAGGACCCAGCTGTGATCCAAAGACAGGAGTCTCACTGTCGCACTTA
CCGGTTTCCAAAGCTCTGGTAGAGGAAGAGTGTGACCCCTGTTGGCCCGAGTAATC
GTCGGATGCGACATACAGGGTTAACAGTAAAGACTGCAAGATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAAACCGCACTTCTCATGGCAGCTTTTGACAGGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTTAAGAAGGGTACAGCTGTG
TTCTGGTACACCTCTGGGAGGGGGAGGTGACTACCGAACAGACATGCTGCCCTGCC
TGTGTTGTGGCTGCAAGTGGCTCCAAATAAGTGGTCCATGACAGGAGACAGGGTTCT
TGAGACCTTGTGGATACACAGAAGTTGACTGACATCTTCTGCTCTCCCTTCTGGTC
CTTCAGCCCATGTCACCGTACAGACAGACACCTTGTATGTTCTTATGTCCTATCAGGCT
GATTTTGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCACTCTGT
GTGACTGAAGTCCCAGCCCTTCATTCAAGCTGTGCCATCCCTGCCCAAGGCTAGGATCA
AAGTGGCTGCAAGAGTTAGCTGCTAGCGCTAGCAAGGTGCCCTTGTACCTCAGGTT
TTAGGTGTGAGATGTTCTGAGAACCAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTTCTATCTATTGTGGCTTACCAAAAATAAAATGTCCTTACAGAAAAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDQAAGFIANLSVQRQFFF
TDEDEIGAAKALMRLQDTRYLDPGTSRGEELPGTKYQAMLSVDCFGMGRSAYNEGDYHHTV
LWMEQVLKQLDAGEEATTIKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEGVKLTPRRKRLF
CRYHHGNRAPQQLIAPFKEEDEWDSPHIVRYYDVMSEDEIERIKEIAPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYVGQQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSSEGDDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCCTTTTGTGGAAAGACAGACCAATAATCCCAGTGTGAGTGAAATTGATTGT
TCATTTATTACCGTTTGCCTGGGTTAGTCGGACACCTTCACTTAAGAGCAGGCAGAAGGAGTGTGA
AGACAGGAACTTCTTCTGGGATGCTGGCTCTGGAAAGCAGCAGGGGCTTGCTCTGTCTTGGCTCATGACC
CAGGTCTCTGGTTAAACTGAAGGCTACTCTGGCTTGCCCATATCATTGATCCTTGAGGGCTGTGCC
CTCTGGGACACCCACGGCCTACACCATGCGACTGAGCTCCCTGTGGCTCTGCTGCCAGGGCTTC
CCTCATCTTAAAGCTGTCTCTGGGCTGAGGGAGGGCCACAGAACATTCAGATTGAGAGCTCGGTAGACCAAAGTG
ATGAAGACTTCAAAACCCGGATGTGCCCCACTACAGGGACCCCACAGGCCATCACAGAAGGTGTCAGGACTC
GGTACATCCACAGACAGGCTGGGCTGGGGTACAGCTGAGCTCTGGCTCTGGACCTCCGGAGCTACACTGTCCA
CTTTGGCCCTGCTGTGAACCGTACCGTGGCCATCACTTCCCTCGGTACTCTACTTCACTGGCAGCGGGGG
CCCGGCTCTCCACAGGAAGGGTCAAGGTGTCTCATGGGATGACGCCCTGGCTCATGTCAAGAGACCTG
GCCACCGTCAACACACTTGGGGGCAACTGAGCTTCTTCACTCATGAGGATGACACATATGCAAGGCC
CCCGGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAAAGCCGGCAGAGGAGTTCATG
GCCAGGCGAGCCGGCTGGACTGTCAAGGGGCTTGGCTACCTGGTGTGAGCTGGCTCTGGCTCTGGCT
GGCACACATCTGGATGGCTCGCAGGAGACATTCTCACTGCCCCCTGGCTGAGGTGGCTGGACCTGGCT
ACTCTCTGGGCTCGGCTGTCTCACAGGACCCAGCAGCTGAGCTGGCTTGAACATGGCCAAAATAGGG
ACCTTGAGAAGGAGGGAGCTCGGCTTCTGGAGTGGAGCAGGCTTAACGTGAAATAGAACACTGCAAGCTCAGA
ACCGGATCCAAACCCGTCAGGGCTCTGGAGTGGAGCTGGAGGCTACAGTGAATAGAACACTGCAAGCTCAGA
TCCGGAACTGACGGCTGCTGGCACCCCGAAGGGGAGCAGGGCTGAGCTGGGCTCTGGCTCTGGCT
CACCAACACTCTGCTTGTGGACTCTTCAACAGACGACACACCTCTCTGTGAGGATGGGG
CTTCCCAAGTGGCCACTACAGGGGCTAGCAGGGGAGCAGCTGGGTGTGGAGACTGGCCCTGGAGCAGCTCA
ATCAGGCTATCACGGCCCTCTGGCTTCAAGAGCAGGAGCTGCTAACAGGCTATGGCCCTGGACCC
GGGGCATGGAGTACCCCTGGACTCTGGTGGAAATGTGACACAGCGTGGGACCCGGCTGGCT
GGGTCACTGGCTGGGGCCACTGAGGCCGGGTGGAAATCCACCTATGCCCTATGTCACTGAGGCCACCCGGAGTGC
ACCTGGTGTCTGCCACTCTGGTGGCTGAAGCTGCTCAGGCCGGCTTCTCTGGAGGCTTGTGAGGACATGTCC
TGGAGCACGAGAACATGCTCACCTGTGCTGGTGTACGGGCACAGAGGTGGCCGTGGAGCTCCAG
ACCCATTCTTGGGTGAAGGCTGAGCAGCGAGGTAGAGCAGCTGGACGGCTGGAGCAGGCTGGCTGGCT
CTGTGAGCAGAGGGCCCTTCCAGTGCGACTCTGGACGTGGTCTCGAAGAAGGACCCCTGTGGACACTCT
TCCTCTTACACCGTGTGGAAGGCCCTGGCCAGCTGGACTCTGGACGTGGTCTCGAAGAATGCCCACCTCT
GGCAGGCCCTCTTCCAGTCTTCACTGGAGTCACTCTGGCCAGCTGGACGAGCTGGCT
CGGGGCTGGCCCTGACCCCCCTCCCTGGCTGACCCCTCCGGGGCTCTTAGGGGGAGATTG
ACCCAGCAGCTCTGGAGGGCTCTCTTCAACACTGACTACCTGGCCGGCCAGCCGGCTGGCA
TGGCAGGCCAGGAAGAGGGAGGGCTGGAGGGCTGGAGGGTGTGGATGATGTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTGGGGCTAGGCCAGGGCTGGTCAAGAGAGTCTCCCTGGAGACTGCAAGCCACGGCTCACTGAAG
AACTCTACACCCGGTGCAGGCCCTGAGAACATAGCACTTAGCCGGCTGGGGGGCTAGGGGGCTGGCCAGCTGG
ACGAGGAGCAGGCCAATAGCACTTAGCCGGCTGGGGGGCTAACCTCATACCTTCTTGTGCTGCT
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAAATTGTTGCTGATTTTTAAATATGAAAATGTTATTAA
ACATGTCCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLI LGSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDEDFKPRIPVYYRDPNKPYKKVLRTRYQTTELGRSERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETLRHLHHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEFIGAGEQARYCHGGFYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLLDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGADETALEQLNRYYQPRRLRFQKQRLLNGYR
RFDPARGMNEYTL DLLLECVTQRGHRRALARRVSLLRPLSRSVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLLVVYGPREGGRRGADPFPFLGVKA AAAAELEERRYPG
TRLAWLA VRAEAPSQVR LMDVVS KKH PVDTLFLLTVWTRGPPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAE GC FYNA DYLAA
RAR LAGELACQEEEEEALEG LVE MDVFLRFSGLHL FRAVE PGLVQKF SLRDCSPRL SEELYHR
CRLSNLEGLGGR AQLAMALF E QEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CAACGTGAGAGGAACCGTGC~~G~~CTGC~~G~~CTTCCTGCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAGCAGCTCCTTTGAAGGGTGTATGCTGG
AA~~G~~CATTTC~~T~~GTGCTT~~G~~ATCACTATGCTAGGACACATTAGGATTGGT~~C~~ATGAA~~A~~
TGCACCACCATGAGCATCATCACCTACAAGCTC~~T~~AA~~C~~AAAAGAAGATATCTGAAAATTC~~A~~
GAGGATGAGCCATGGAGCTAGTAAGAGCTT~~C~~GAGTATACTGTATTATC~~T~~GTAAA~~C~~
CAAAGATGTGAGCTTGGCTGCAGTAAGGAGACTTGACCAACACTGTGACAA~~G~~CAG
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTC~~A~~TTAATATGGACACAA~~A~~ATGACATG
TGGTTAATGATGAGAAAAGCTTACA~~A~~ACGCTT~~G~~TATAAGTATAGAGACCAATACACTG
GTTCTTCTTGCACGCC~~C~~ACTACGTT~~G~~TATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACGC~~T~~TCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCA~~A~~GTAAAAGACTTACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGTTGGAAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGA~~A~~ATATGCTGGAGTAT~~T~~GCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCA~~A~~TGTGTTGGCTTCTATTAAAGGAGCAATGACTTATCACCC
CAAC~~C~~AGGTACTAGAAGGCTTGT~~C~~AGATATGGCT~~G~~TACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGC~~T~~TAGGGCAT~~T~~GGG~~C~~ATTTCAAT
GATGCATTGGTTCTTACCT~~C~~AAATGGTCTGACAATGACTGAGAAGTGGTAGAAAGCG
TGAATATGATTTGTATAGGACGTGTGTTGTCATTATTGTAGTAGTA~~A~~CTACATAT~~CC~~AA
TACAGCTGTATGTTCTTTCTTA~~T~~GGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTAC~~T~~TTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGTAATG
TGTGGAAAGAAGTGT~~T~~TAAGAATAATA~~T~~TTGCAAA~~A~~ACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAATCTG~~T~~GGGCACATATT~~T~~TG~~T~~GATTGGTT
AAAAAAATTAAACAGGTCTTAGC~~G~~TCTAAGATATGCAAA~~A~~GTATCTCTAGTTGTGAATT
TGTGATTAAAGTAAA~~A~~CTTGTGTTCC~~T~~TACTTCTAA~~T~~ACTGATT~~T~~TGTTCT
AAGCCTCCCAAGTCCAATGGATTG~~C~~TTCTCAAA~~A~~GTACA~~A~~CTAAGCAACTAAAGAAA
ATTAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPHQGMIWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCGATCTTACCAACAAAACACTCCTGAGGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAAACAAAAACCAAAGAGAGAGAGAAAAA**ATGAATT**CATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGGATGTTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTCATCACAGATGTGTTGTGACATTGCGAT
CTTCAAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTCAGAGCTCCTGCT
ACAATTATGGATCAGGTTCACTGAGAAATTGTTGTCATTGAACGGAAATTTCATCC
AGCTGCTACTTCTTTCTACTGACACCAATTCCCTGGGCTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGGATGTAGGGGAGCCAAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTAAGTAGGAAATAATCCTTG
AACAAAGGAAAATCTCTT**AA**GAACAGAACAGGACAACTCAAATGTGTAAGAAGGAAGAGCA
AGAACATGGCCACACCCACGGCCCCACAGAGAAATTGTCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGSLS

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDASALYRCEVVARNDRK
EIDEIVIELTVQVKPVTCPVCRVPKAQPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPFRNRNSSFHLNSETGTLVFTAHHKDDSGQQYCIASNDAGSARCEEQEMEVYDLDNIGGIIGG
VLVVLAVLALITLGICCAYRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267